
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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ch_nn      n.a. - n.a. database search, using Smith-Waterman algorithm
Run on:    Tue Dec 8 20:49:12 1998; MasPar time 2424.36 Seconds
           1535.342 Million cell updates/sec

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Title: >US-08-963-656-1
Description: (1-1689) from US08963656.seq
Perfect Score: 1688
N.A. Sequence: 1 AATCCCTTTTCTCGGACCTC.....CCCTGCTTATGAAAAGCTT 1689
Comp: TTAGAAAAGGACGGCTGTGAG.....GGACGAAATTACTTTTCGAA

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Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 567134 seqs, 1101898692 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb155

1:em_ba 2:em_fun 3:em_btg 4:em_hum1 5:em_hum2 6:em_in
7:em_on 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl
13:em_ro 14:em_vi
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21:gb_pat 22:gb_ph 23:gb_pl1 24:gb_pl2 25:gb_pr1
26:gb_pr2 27:gb_pr3 28:gb_ro 29:gb_st 30:gb_sts 31:gb
32:gb_un 33:gb_vl

Statistics: Mean 11.614: Variance 5.488: scale 2.116

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.	
1	1686	99.9	1689	25	HSU49727	Human C-C chemokine re	0.00e+00
2	1637	97.0	1717	25	HSU51241	Human eosinophil ectox	0.00e+00
3	1183	70.1	1201	27	HSU28694	Human eosinophil CC ch	0.00e+00
4	1064	63.0	1068	26	AF026535	Homo sapiens chemokine	0.00e+00
5	958	56.8	1068	26	CAY13775	Cercopithecus aethiops	0.00e+00
6	952	56.4	1068	26	MMY13776	Macaca mulatta CCR-3 g	0.00e+00
7	948	56.2	1068	26	AF017283	Macaca mulatta chemoki	0.00e+00
8	600	35.5	1440	28	MMU28406	Mus musculus macrophag	0.00e+00
9	570	33.8	1185	28	MMU29677	Mus musculus chemokine	0.00e+00
10	558	33.1	1315	28	RNRPCR3	Rattus norvegicus mRNA	0.00e+00
11	551	32.6	1080	28	AF003954	Rattus norvegicus chem	0.00e+00
12	424	25.1	1495	25	HUMCCCKRIA	Human C-C chemokine re	0.00e+00
13	424	25.1	1609	21	E13385	cdNA encoding human MI	0.00e+00

14	424	25.1	2156	21	I58541	Sequence 1 from patent	0.00e+00
15	424	25.1	2156	25	HUMR145	Homo sapiens macrophag	0.00e+00
16	424	25.1	2214	26	HUMH145	Human mRNA for HM145	0.00e+00
17	383	22.7	1068	26	AF017282	Macaca mulatta chemoki	2.64e-301
18	355	21.0	1544	21	E13732	cDNA encoding rat CC c	2.41e-276
19	349	20.7	1748	28	MMU28404	Mus musculus macrophag	5.27e-271
20	347	20.6	1068	28	MMU29678	Mus musculus chemokine	3.17e-269
21	272	16.1	1371	28	MMU28405	Mus musculus macrophag	8.81e-203
22	264	15.6	184427	33	EHVU20824	Equine herpesvirus 2,	9.84e-196
23	265	14.0	1457	28	RNCRK5	R.norvegicus mRNA for	3.82e-171
24	236	14.0	1689	28	RNU77350	Rattus norvegicus chem	3.82e-171
25	229	13.6	1059	26	AF005661	Macaca nemestrina CC c	5.11e-165
26	229	13.6	1059	27	MMU96762	Macaca mulatta chemoki	5.11e-165
27	230	13.6	1078	28	AF022990	Mus musculus CC chemok	6.82e-166
28	230	13.6	2888	28	D83648	House mouse; Musculus	6.82e-166
29	228	13.5	1060	26	AF011530	Homo sapiens isolate U	3.83e-164
30	228	13.5	1125	28	MMU47036	Mus musculus MIP-1 alp	3.83e-164
31	225	13.3	1059	26	AF005658	Papio hamadryas CC che	1.60e-161
32	225	13.3	1059	26	AF005660	Macaca fascicularis CC	1.60e-161
33	225	13.3	1059	26	AF023452	Papio hamadryas anubis	1.60e-161
34	225	13.3	1059	26	AF005662	Macaca mulatta CC chem	1.60e-161
35	225	13.3	1059	27	MMU73739	Macaca mulatta CC chem	1.60e-161
36	224	13.3	1059	26	AF005659	Gorilla gorilla CC che	1.20e-160
37	224	13.3	1059	26	AF005663	Pan troglodytes CC che	1.20e-160
38	224	13.3	1060	26	AF011509	Homo sapiens isolate K	1.20e-160
39	224	13.3	1060	26	AF011513	Homo sapiens isolate M	1.20e-160
40	224	13.3	1060	26	AF011519	Homo sapiens isolate T	1.20e-160
41	224	13.3	1060	26	AF011526	Homo sapiens isolate U	1.20e-160
42	225	13.3	1078	28	MMU83327	Mus musculus CC chemok	1.60e-161
43	225	13.3	1086	27	CAU83324	Cercopithecus aethiops	1.60e-161
44	225	13.3	1966	27	MMU77672	Macaca mulatta CC chem	1.60e-161
45	223	13.2	1059	27	AF051907	Cercopithecus torquatus a	8.95e-160

ALIGNMENTS

1	RESULT	HSU49727	1689 bp	DNA	PRI	04-OCT-1996
	LOCUS	Human C-C chemokine receptor 3 (CCR-3) gene, complete cds.				
	DEFINITION	U49727				
	ACCESSION	NID	g1477560			
	KEYWORDS					
	SOURCE	human.				
	ORGANISM	Homo sapiens				
		Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;				
		Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	REFERENCE	1 (bases 1 to 1689)				
	AUTHORS	Ponath,P.D., Qin,S., Post,T.W., Wang,J., Wu,L., Gerard,N.P., Newman,W., Gerard,C. and Mackay,C.R.				
		Molecular cloning and characterization of a human eotaxin receptor expressed selectively on eosinophils				
	TITLE	J. Exp. Med. 183 (6), 2437-2448 (1996)				
	JOURNAL	96281895				
	MEDLINE	2 (bases 1 to 1689)				
	REFERENCE	Ponath,P.D.				
	AUTHORS	Direct Submission				
	TITLE	Submitted (21-FEB-1996) Paul D. Ponath, Molecular Biology,				
	JOURNAL	LeukoSite, Inc., 215 First St., Cambridge, MA 02118, USA				

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and MCP-3"
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REFERENCE 2 (bases 1 to 1717)
AUTHORS Daugherty, B.L.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-1996) Bruce L. Daugherty, Inflammation Research,
Merck Research Laboratories, R80W-107, P.O. Box 2000, Rahway, NJ
07065, USA

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BASE COUNT 434 a 428 c 351 g 504 t
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Qy 1 AATCCTTTCTGGCACCCTCTGATAT - CTTTGAATTCATGTTAAAGATCCCTAGCG 59
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Qy 60 TGCTATCATATGGCATCTTTGTTGAGTACATGATTAATCACTGGTGTGTTTACGA 119
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1615 TTTTTCACAAATACAAATAGTAACTATTTTATTTTCTTAATGTTGCTAGTCTTCTTCCCTG 1674
1703 CTTAATGAAGCTT 1717

QY 1675 CTTAATGAAGCTT 1689

RESULT 3
LOCUS HSU28694 1201 bp mRNA PRI 16-MAY-1996
DEFINITION Human eosinophil CC chemokine receptor 3 mRNA, complete cds.
ACCESSION U28694
NID 91199579

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;
TITLE Vertebrata; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1200)

REFERENCE 2
AUTHORS Combadiere, C., Ahuja, S.K. and Murphy, P.M.
TITLE Cloning and functional expression of a human eosinophil CC
chemokine receptor
J. Biol. Chem. 270 (28), 16491-16494 (1995)

REFERENCE 3
AUTHORS Combadiere, C., Ahuja, S.K. and Murphy, P.M.
TITLE Cloning and functional expression of a human eosinophil CC
chemokine receptor
J. Biol. Chem. 271 (18), 11034 (1996)

REFERENCE 4
AUTHORS Combadiere, C.
TITLE Direct Submission
Submitted (07-JUN-1995) Christophe Combadiere, NIAID, National
Institutes of Health, Building 10, Room 11N11, Bethesda, MD 20892,
USA

COMMENT
On Feb 22, 1996 this sequence version replaced gi:881569.
[Erratum J. Biol. Chem. 270 (1995) 30235].

FEATURES
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BASE COUNT 278 a 320 c 267 g 336 t

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Matches 1197; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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QY 210 CTTTGGTACACATCCTACTATGATGAGTGGGCTGCTGTGTGAAAAGCTGATACAG 269

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QY 270 AGCACTGATGCGCCAGTTGTGCGCCCGCTGCTACTCCCTGGTGTCTACTGTGGCCCTCT 329

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Db 1200 GT 1201
QY 1349 GT 1350

RESULT 4
LOCUS AF026535 1068 bp mRNA PRI 02-NOV-1997
DEFINITION Homo sapiens chemokine receptor (CCR3) mRNA, complete cds.
ACCESSION AF026535
NID 92582565

KEYWORDS
SOURCE

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL.

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

5

[illegible]

ORIGIN

Query Match

Best Local

Matches 10

[illegible]

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181 ATGA

31

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Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1068)
Xiao, L., Weiss, S., Qari, S., Rudolph, D., Hodge, T. and Lal, R.
Partial resistance to infection by syncytium-inducing primary HIV-1
in exposed uninfected individuals homozygous for CCR5 32bp deletion
Unpublished
2 (bases 1 to 1068)
Qari, S.
Direct Submission
Submitted (24-SEP-1997) Retrovirus Diseases Branch, Centers for
Disease Control and Prevention, 1600 Clifton Road, Atlanta, GA
30333, USA

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301 TACTCCCTGGTGTTCATGCTGGGCTCTTGGGCAATGTTGGTGGTATGATCTCAT 360
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1021 TCTGTCT 1068
1201 TCTGTCT 1248

RESULT 7 AF017283 1068 bp DNA PRI 18-SEP-1997
LOCUS Macaca mulatta chemokine receptor (CCR3) gene, complete cds.
DEFINITION
ACCESSION AF017283
NID 92407218

KEYWORDS
SOURCE ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
gene
CDS
BASE COUNT 229 a 289 c 245 g 305 t
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Query Match 56.2%; Score 948; DB 26; Length 1068;
Best Local Similarity 94.4%; Pred. No. 0.00e+00;
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1021 TCTGTCT 1068
1201 TCTGTCT 1248

rhesus monkey.
Macaca mulatta
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
1 (bases 1 to 1068)
Hauer, D.A., Margulies, B.J. and Clements, J.E.
Direct Submission
Submitted (05-AUG-1997) Division of Comparative Medicine, Johns
Hopkins University School of Medicine, 720 Rutland Ave., Traylor
G-60, Baltimore, MD 21205, USA
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229 a 289 c 245 g 305 t

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RESULT 8
LOCUS MMU28406 1440 bp DNA 27-FEB-1996
DEFINITION Mus musculus macrophage inflammatory protein-1 alpha receptor-like
2 gene, complete cds.
ACCESSION U28406
NID g1203800
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1440)
Gao, J. L. and Murphy, P. M.
Vertebrate; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
1 (bases 1 to 1440)
Gao, J. L. and Murphy, P. M.
Cloning and differential tissue-specific expression of three mouse
beta chemokine receptor-like genes, including the gene for a
functional macrophage inflammatory protein-1 alpha receptor
J. Biol. Chem. 270 (29), 17494-17501 (1995)
95340546
MEDLINE 2 (bases 1 to 1440)
REFERENCE Gao, J. L.
AUTHORS Direct Submission
TITLE National Institutes of Health, Building 10, Room 1N113, Bethesda,
MD 20892, USA
JOURNAL
COMMENT On Feb 27, 1996 this sequence version replaced gi:1199860.
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CDS

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DEFINITION	Human C-C chemokine receptor type 1 (C-C CKR-1)		31-DEC-1994
ACCESSION	L09230		
NID	g179984		
KEYWORDS	C-C chemokine receptor type 1.		
SOURCE	Homo sapiens cDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Neote, K., DiGregorio, D., Mak, J.Y., Horuk, R. and Schall, T.J.		
TITLE	Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor		
JOURNAL	Cell 72 (3), 415-425 (1993)		
MEDLINE	93161416		
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g292416
G-protein activator; G-protein coupled receptor; RANTES receptor;
macrophage inflammatory protein-1-alpha.
Homo sapiens (library: 2 kb HL-60 neutrophil cDNA in lambda-ZAP)
cDNA to mRNA.
Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (Bases 1 to 2156)
Gao, J.-L., Tiffany, H.L., Kuhns, D., McDermott, D., Li, X., Francke, U.
and Murphy, P.M.
Structure and functional expression of the human macrophage
inflammatory 1 alpha (MIP-1alpha)/RANTES receptor
J. Exp. Med. 177, 1421-1427 (1993)
93240122

Location/Qualifiers
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BASE COUNT 538 a 547 c 504 g 567 t
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Best Local Similarity 71.9%; Pred. No. 0.00e+00;
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WQISREH

(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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ch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Dec 8 13:14:19 1998; MasPar time 11.57 Seconds
Tabular output not generated. 496.409 Million cell updates/sec

Title: >US-08-963-656-2
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Perfect Score: 2765
Sequence: 1 MTTSLDIVEFGTTSYDDV.....LERTSSVSPSTAEPELSIVF 355

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

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1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 34.824; Variance 168.421; scale 0.207

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description	Pred. No.
1	2751	99.5	355	19 W03376	CC-chemokine receptor	1.42e-228
2	2751	99.5	355	23 W10100	Human C-C chemokine r	1.42e-228
3	2748	99.4	355	28 W31850	Human eosinophil eota	2.62e-228
4	2748	99.4	355	24 W27124	Human chemokine recep	2.62e-228
5	2748	99.4	355	19 W03377	CC-chemokine receptor	2.62e-228
6	2710	98.0	356	26 W25943	Human CCR3 chemokine	6.22e-225
7	2658	96.1	355	19 W03378	CC-chemokine receptor	2.58e-220
8	1828	66.1	355	11 R52749	C-C chemokine recepto	8.66e-147
9	1828	66.1	355	25 W26588	Human MIP-1 alpha/RAN	8.66e-147
10	1828	66.1	355	24 W25751	Human MIP-1alpha/RANT	8.66e-147
11	1720	62.2	355	24 W29179	Rat CC chemokine rece	2.96e-137
12	1509	54.6	352	24 W27125	Macaque chemokine rec	1.17e-118
13	1496	54.1	352	24 W27123	Human chemokine recep	1.63e-117
14	1496	54.1	352	27 W27407	Human CCR5	1.63e-117
15	1496	54.1	352	29 W23834	Human CC chemokine re	1.63e-117
16	1497	54.1	371	29 W23834	Human CC chemokine re	1.63e-117
17	1483	53.6	352	20 W07602	Human G-protein chemo	2.27e-116
18	1438	52.0	360	14 R79166	Human monocyte chemoa	2.06e-112

11995

19	1438	52.0	360	26 W35833	Human monocyte chemoa	2.06e-112
20	1390	50.3	332	28 W26766	Human chemokine recep	3.41e-108
21	1352	48.9	374	14 R79165	Human monocyte chemoa	7.43e-105
22	1251	45.2	360	19 R99274	Chemokine receptor K5	5.40e-96
23	1079	39.0	355	20 W07618	Human G-protein recep	6.04e-81
24	1006	36.4	355	11 R53748	Seven transmembrane r	1.41e-74
25	934	33.8	356	29 W48087	Human macrophage/dend	2.60e-68
26	921	33.3	344	28 W26767	Human chemokine recep	3.51e-67
27	816	29.5	358	11 R53745	Partial sequence of s	4.46e-58
28	816	29.5	410	11 R53743	Putative seven trans	4.46e-58
29	813	29.4	378	11 R53744	Putative seven trans	8.11e-58
30	804	29.1	184	27 W27406	Inactive human CCR5	4.87e-57
31	804	29.1	215	27 W27408	Inactive human CCR5	4.87e-57
32	793	28.7	365	29 W48086	Human dendritic cell	4.35e-56
33	787	28.5	378	10 R54079	Epstein Barr virus in	1.43e-55
34	756	27.3	359	11 R53747	Seven transmembrane r	6.81e-53
35	738	26.7	355	7 R33420	Human IL-8 receptor f	2.43e-51
36	738	26.7	360	15 R80758	Interleukin 8 recepto	2.43e-51
37	738	26.7	1064	14 R70124	Sequence in a low aff	2.43e-51
38	738	26.7	360	6 R28273	IL8-R type 2-GBP 130	2.43e-51
39	724	26.2	350	15 R80951	Recombinant high affi	3.90e-50
40	724	26.2	350	12 R68811	Interleukin-8 recepto	3.90e-50
41	724	26.2	350	13 R80756	Interleukin-8 recepto	3.90e-50
42	724	26.2	415	23 W19780	Human G-protein chemo	3.90e-50
43	724	26.2	1060	14 R70123	IL8-R type 1-GBP 130	3.90e-50
44	720	26.0	360	15 R80953	Recombinant high affi	8.61e-50
45	717	25.9	350	5 R27791	Interleukin-8 recepto	1.56e-49

ALIGNMENTS

RESULT 1
ID W03376 standard; Protein: 355 AA.
AC W03376;
DT 15-NOV-1996 (first entry)
DE CC-chemokine receptor 3;
KW CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;
KW antiinflammatory; eosinophil.
OS Homo sapiens.
FH Key Location/Qualifiers
FT region 130..138
FT /note= "amino acids 130-138 comprise a motif
FT conserved among C-X-C and C-C chemokine
FT receptors"

W09622371-A2.
PD 25-JUL-1996.
PF 19-JAN-1996; U00608.
PR 19-JAN-1995; US-375199.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (LEUK-) LEUKOSITE INC.
PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
PI Qin S;
PI WPI; 96-354528/35.
DR N-PSDB; T31334.
PT Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
PS Claim 10; Page 110-111; 153pp; English.
CC A novel human receptor (W03376), designated Eos L2 or C-C chemokine
CC receptor 3 (CCR-3), is involved in leukocyte migration associated
CC with inflammation. Its sequence was deduced from a genomic DNA
CC clone (T31334). A slightly different amino acid sequence (W03377)
CC was deduced from a cDNA clone (T31335) and a consensus sequence
CC is given in W03378. Recombinant CCR-3 can be produced in host
CC cells, and is useful for screening for CCR-3 ligands, promoters
CC and inhibitors. The inhibitors can be used to treat inflammatory
CC disease.
SQ Sequence 355 AA;
Query Match 99.5%; Score 2751; DB 19; Length 355;
Best Local Similarity 99.7%; Pred. No. 1.42e-228;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 mtsldtvetfqttsydvdlcekadtralmavfpplyslvftvgllgnvvvmili 60
 Qy 1 MTSLSLDTVETFGTTSYDDVGLCEKADTRALMAQFVPPPLYSLVFTFGLLGNVVVMILI 60
 Db 61 kyririntniylnlaisdlflvtlpfwhvyrghnwvfhgmckllsgfyhtglyse 120
 Qy 61 KYRRLRINTNIYLLNLAISDLLFLVTFWVHYVGRHNWVFGHGMCKLLSGFYHTGLYSE 120
 Db 121 iffiilltidrylaivhavfalrartvtfvgitsvwtglavlaalpefifeteelfee 180
 Qy 121 IFFIILLTIDRYLAIVHAVFALRARTVTFGVITSVWTGLAVLAALPEFIFYETEELFEE 180
 Db 181 tlcsalypedtvyswrhfhltmrtifclvlpplvmaicytgiiktlrcpskkykairl 240
 Qy 181 TLCSALYPEDTVYSWRHFHLMRTMRTIFCLVLPPLVMAICYTGIKTLRCPSKKYKAIRL 240
 Db 241 ifvimaavffitwpyvnaillssyqsilfngdcertkhlldvmlvteviayshccmpvi 300
 Qy 241 IFVIMAVFFITWPPYNVAILSSYQSILFNGDCERTKHLDLVMLVTEVIAYSHCCMPVI 300
 Db 301 yafvgerfkrlyrhffrhlmlhlgryipflpseklerstssvstaeplsivf 355
 Qy 301 YAFVGERFKRKYLRHFFRHLMLHLGRYPFLPSEKLERSTSSVSPSTAEPLSIVF 355

RESULT 2

ID W10100 standard; Protein: 355 AA.

AC W10100;
 DT 30-SEP-1997 (first entry)
 DE Human C-C chemokine receptor 3.
 KW Human; eotaxin; eosinophil; chemoattractant; stimulation;
 KW accumulation; attraction; chemotaxis; diagnosis; prevention;
 KW treatment; disease; inflammation; allergy; asthma; rhinitis;
 KW hypersensitivity; lung; pneumonia; Loeffler's; syndrome;
 KW interstitial; ILD; idiopathic pulmonary fibrosis;
 KW rheumatoid arthritis; systemic; lupus erythematosus; SLE;
 KW ankylosing spondylitis; sclerosis; Sjogren's; polymyositis;
 KW dermatomyositis; bowel; anaphylaxis; drug; penicillin;
 KW cephalosporin; insect sting; Crohn's; ulcerative colitis;
 KW spondyloarthropathy; scleroderma; psoriasis; dermatosis;
 KW dermatitis; eczema; atopic; urticaria; necrotising; cutaneous;
 KW vasculitis; myositis; fascitis; multiple sclerosis;
 KW myasthenia gravis; juvenile onset diabetes; glomerulonephritis;
 KW autoimmune; thyroiditis; Bechet's; graft; rejection;
 KW transplantation; allograft; graft versus host; cancer;
 KW leukocyte infiltration; reperfusion injury; atherosclerosis;
 KW haematologic malignancy; septic; endotoxic; shock;
 KW polymyositis; dermatomyositis; immunosuppression; immunodeficiency;
 KW AIDS; radiation therapy; chemotherapy; autoimmune; corticosteroid;
 KW C-C chemokine receptor 3; CRK3.
 KW Homo sapiens.
 PW W09700960-A1.
 PD 09-JAN-1997.
 PE 21-JUN-1996; U10723.
 PR 23-JUN-1995; US-494093.
 PA (LEUK-) LEUKOSITE INC.
 PI Mackay C, Newman W, Ponath PD, Qin S, Ringler DJ;
 DR N-PSDB; T58783.
 DR WPI; 97-087387/08.
 PT New isolated human eotaxin gene - used to develop prods. for the
 PT diagnosis and treatment of e.g. inflammation, allergies, auto-immune
 PT disease, infections and tumours
 PS Example 7; Pages 98-99; 130pp; English.
 CC The present sequence is human C-C chemokine receptor 3 (CRK3),
 CC to which human eotaxin (hE), an eosinophil specific chemoattractant
 CC capable of stimulating eosinophil accumulation and/or attracting
 CC eosinophils (including chemotaxis), binds.
 CC hE can be used to develop products for the diagnosis, prevention or
 CC treatment of hE associated diseases or conditions. The products can
 CC be used to treat inflammatory or allergic diseases and conditions,
 CC including respiratory allergic diseases (e.g. asthma, allergic
 CC rhinitis, hypersensitivity lung diseases or pneumonia, allergic

CC eosinophilic pneumonias such as Loeffler's syndrome and chronic
 CC eosinophilic pneumonia, interstitial lung diseases (ILD) such as
 CC idiopathic pulmonary fibrosis or ILD associated with rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), ankylosing
 CC spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis
 CC or dermatomyositis), systemic anaphylaxis or hypersensitivity
 CC responses, drug allergies (e.g. to penicillin and cephalosporins),
 CC insect sting allergies, inflammatory bowel diseases (e.g. Crohn's
 CC disease and ulcerative colitis), spondylarthropathies,
 CC scleroderma, psoriasis and inflammatory dermatoses (e.g.
 CC dermatitis, eczema, atopic dermatitis, allergic contact dermatitis,
 CC urticaria and necrotising, cutaneous and hypersensitivity
 CC vasculitis), eosinophilic myositis and fascitis, multiple
 CC sclerosis, SLE, myasthenia gravis, juvenile onset diabetes,
 CC glomerulonephritis, autoimmune thyroiditis, Bechet's disease, graft
 CC rejection (e.g. in transplantation) including allograft rejection or
 CC graft versus host disease and cancers with leukocyte infiltration
 CC of the skin or organs. The products can also be used to treat other
 CC diseases or conditions requiring the inhibition of undesirable
 CC inflammatory responses, including reperfusion injury,
 CC atherosclerosis, certain haematologic malignancies, cytokine
 CC induced toxicity (e.g. septic or endotoxic shock), polymyositis,
 CC dermatomyositis, immunosuppression (e.g. in individuals with
 CC immunodeficiency syndromes such as AIDS, undergoing radiation
 CC therapy, chemotherapy, therapy for autoimmune disease or other drug
 CC therapy, such as corticosteroid therapy, which causes
 CC immunosuppression), immunosuppression due to (e.g. congenital)
 CC deficiency (e.g. in eotaxin) or infectious diseases such as parasitic
 CC diseases.
 CC Degenerate primers based on the guinea pig eotaxin amino acid
 CC sequence were used for the reverse transcriptase polymerase chain
 CC reaction (RT-PCR) amplification of RNA isolated from inflamed,
 CC eosinophilic lung tissue obtained from Balb/c mice sensitised to
 CC ovalbumin. The amplification product was used as a probe to screen
 CC a human genomic library in vector EMBL3 SP6/T7 to obtain the hE
 CC gene.
 SQ Sequence 355 AA;

Query Match 99.5%; Score 2751; DB 23; Length 355;
 Best Local Similarity 99.7%; Pred. No. 1.42e-228;
 Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 mtsldtvetfqttsydvdlcekadtralmavfpplyslvftvgllgnvvvmili 60
 Qy 1 MTSLSLDTVETFGTTSYDDVGLCEKADTRALMAQFVPPPLYSLVFTFGLLGNVVVMILI 60
 Db 61 kyririntniylnlaisdlflvtlpfwhvyrghnwvfhgmckllsgfyhtglyse 120
 Qy 61 KYRRLRINTNIYLLNLAISDLLFLVTFWVHYVGRHNWVFGHGMCKLLSGFYHTGLYSE 120
 Db 121 iffiilltidrylaivhavfalrartvtfvgitsvwtglavlaalpefifeteelfee 180
 Qy 121 IFFIILLTIDRYLAIVHAVFALRARTVTFGVITSVWTGLAVLAALPEFIFYETEELFEE 180
 Db 181 tlcsalypedtvyswrhfhltmrtifclvlpplvmaicytgiiktlrcpskkykairl 240
 Qy 181 TLCSALYPEDTVYSWRHFHLMRTMRTIFCLVLPPLVMAICYTGIKTLRCPSKKYKAIRL 240
 Db 241 ifvimaavffitwpyvnaillssyqsilfngdcertkhlldvmlvteviayshccmpvi 300
 Qy 241 IFVIMAVFFITWPPYNVAILSSYQSILFNGDCERTKHLDLVMLVTEVIAYSHCCMPVI 300
 Db 301 yafvgerfkrlyrhffrhlmlhlgryipflpseklerstssvstaeplsivf 355
 Qy 301 YAFVGERFKRKYLRHFFRHLMLHLGRYPFLPSEKLERSTSSVSPSTAEPLSIVF 355

RESULT 3

ID W31850 standard; Protein: 355 AA.

AC W31850;
 DT 07-MAY-1998 (first entry)
 DE Human eosinophil eotaxin receptor protein CC CRK3.
 KW Eosinophil eotaxin receptor; CC CRK3; human; treatment; dermatitis;

KW atopic condition; allergic rhinitis; conjunctivitis; bronchial asthma;
 KW beta-chemokine receptor; viral infection.
 OS Homo sapiens.
 PN W09741154-A1.
 PD 06-NOV-1997. U06568.
 PR 24-APR-1997; PF 17-JAN-1997; GB-000894.
 PR 26-APR-1996; US-016158.
 PR 26-APR-1996; US-017113.
 PA (MERI) MERCK & CO INC.
 PI Daugherty BL, Demartino JA, Siciliano SJ, Springer MS;
 PI WPI; 97-549685/50.
 DR N-PSDB; T93601.
 PT New isolated human eosinophil eotaxin receptor - used to develop
 PT products for treating and preventing atopic conditions e.g. allergic
 PT rhinitis, dermatitis, conjunctivitis and bronchial asthma
 PT Claim 5: Page 15; 51pp; English.
 CC This is a human eosinophil eotaxin receptor. The 5099 base pair encoding
 CC cDNA sequence comprises a 1065 base pair open reading frame encoding this
 CC 355 amino acid eosinophil eotaxin receptor protein, flanked by a 5',
 CC genomic DNA sequence and a 3' terminator region. This novel eosinophil
 CC eotaxin receptor is a human beta-chemokine receptor designated CC KR3.
 CC Agents which bind to this eosinophil eotaxin receptor can be used for
 CC the treatment and prevention of atopic conditions such as allergic
 CC rhinitis, dermatitis, conjunctivitis and bronchial asthma. Agents which
 CC block this eosinophil eotaxin receptor can be used to prevent viral
 CC infection in healthy individuals and slow or halt viral progression
 CC in infected patients.
 SQ Sequence 355 AA;

Query Match 99.4%; Score 2748; DB 28; Length 355;
 Best Local Similarity 99.4%; Pred. No. 2.62e-228;
 Matches 353; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 mtsldtvetftgtsydyddvgllcekadtralmagfvpplyslvftvlglnvmmvmlil 60
 QY 1 MTSLSLDTVETFTGTSYDYDDVGLLCEKADTRALMAQFVPPPLYSLVFTVGLGNNVVMVILI 60
 Db 61 kyrllrimtniylnlaisdlflvltplfwihyvrghnvwfghgmckllsgfyhtglyse 120
 QY 61 KYRRLRIMTNIYLLNLAISDLFLVLTPLFWIHVYVRGHNVWFGHGMCKLLSGFYHTGLYSE 120
 Db 121 iffiilltdridylaivhavfaiarlartvfgitsvltwglavlaalpefifeteelfee 180
 QY 121 IFFIILLTIDRILAIVHAVFALRARTVFGITSVLTWGLAVLAALPEFIFETEELFEE 180
 Db 181 tlcsalypedtyvswrhhftrmtifclvlpvlmaicytgiiktlrcpskkykairl 240
 QY 181 TLCSALYPEDTYVSWRHHFTRMTIFCLVLPVLVMAICYTGIKTLRCPSKKYKAIRL 240
 Db 241 ifvimaaffifwtpynvallsyqsilfgndcerskhlldvmlvteviayshccmnpvi 300
 QY 241 IFVIMAFFIFWTPYNVALLSSYQSILFGNDCERTKHLDLVMLVTEVIAYSHCCMNPVI 300
 Db 301 yafvgerfrkylrhffhrlhmlhlgryipfipseklertssvspstaepelsivf 355
 QY 301 YAFVGERFRKYLRRHFFRHLHMLHGRYPFIPSEKLERTSVSSVSPSTAEPELSIVF 355

RESULT 4
 ID W27124 standard; Protein; 355 AA.
 AC W27124;
 DT 14-DEC-1997 (first entry)
 DE Human chemokine receptor 88-2B.
 KW Chemokine receptor 88-2B; atherosclerosis; rheumatoid arthritis;
 KW tumour; asthma; viral infection; AIDS; inflammation;
 KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
 KW G protein coupled receptor; ligand; modulator; antibody; human.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..36
 FT domain /label= Extracellular_domain
 FT domain 60..71

FT domain /label= Intracellular_domain
 FT 93..107
 FT domain /label= Extracellular_domain
 FT 131..151
 FT domain /label= Intracellular_domain
 FT 171..196
 FT domain /label= Extracellular_domain
 FT 219..240
 FT domain /label= Intracellular_domain
 FT 263..284
 FT domain /label= Extracellular_domain
 FT 306..355
 FT domain /label= Intracellular_domain
 PN W09722698-A2.
 PD 26-JUN-1997. U20759.
 PF 20-DEC-1996; U20759.
 PR 07-JUN-1996; US-661393.
 PR 20-DEC-1995; US-575967.
 PA (ICOS-) ICOS CORP.
 PI Gray PW, Raport CJ, Schweickart VL;
 PI WPI; 97-341689/31.
 DR N-PSDB; T85162.
 PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used
 PT to modulate leukocyte trafficking, e.g. for treatment of
 PT inflammation, tumours, viral infections, autoimmune diseases, etc.
 PS Claim 1: Page 50-51; 65pp; English.
 CC This polypeptide sequence comprises novel human chemokine receptor
 CC 88-2B, a G protein coupled receptor that is involved in leukocyte
 CC trafficking. Its amino sequence was deduced from a cDNA clone
 CC (T85162) isolated from a macrophage library. It shows 72% identity
 CC to CCKR1. Chemokine receptor 88C (see W27123) has also been
 CC identified. 88C and 88-2B receptors and their polypeptide fragments
 CC can be produced in transformed host cells. The receptors, peptides
 CC comprising one or more of the extracellular or intracellular
 CC domains, and anti-receptor antibodies can be used to modulate
 CC receptor activities, particularly ligand and G protein binding, and
 CC are potentially useful in the treatment of
 CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune
 CC response, abnormal haematopoietic processes etc.
 SQ Sequence 355 AA;

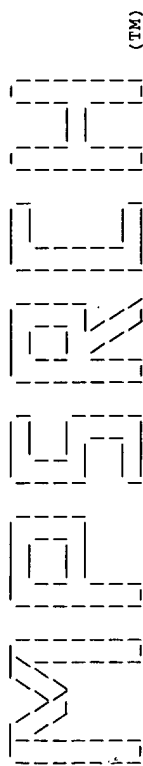
Query Match 99.4%; Score 2748; DB 24; Length 355;
 Best Local Similarity 99.4%; Pred. No. 2.62e-228;
 Matches 353; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 1 mtsldtvetftgtsydyddvgllcekadtralmagfvpplyslvftvlglnvmmvmlil 60
 QY 1 MTSLSLDTVETFTGTSYDYDDVGLLCEKADTRALMAQFVPPPLYSLVFTVGLGNNVVMVILI 60
 Db 61 kyrllrimtniylnlaisdlflvltplfwihyvrghnvwfghgmckllsgfyhtglyse 120
 QY 61 KYRRLRIMTNIYLLNLAISDLFLVLTPLFWIHVYVRGHNVWFGHGMCKLLSGFYHTGLYSE 120
 Db 121 iffiilltdridylaivhavfaiarlartvfgitsvltwglavlaalpefifeteelfee 180
 QY 121 IFFIILLTIDRILAIVHAVFALRARTVFGITSVLTWGLAVLAALPEFIFETEELFEE 180
 Db 181 tlcsalypedtyvswrhhftrmtifclvlpvlmaicytgiiktlrcpskkykairl 240
 QY 181 TLCSALYPEDTYVSWRHHFTRMTIFCLVLPVLVMAICYTGIKTLRCPSKKYKAIRL 240
 Db 241 ifvimaaffifwtpynvallsyqsilfgndcerskhlldvmlvteviayshccmnpvi 300
 QY 241 IFVIMAFFIFWTPYNVALLSSYQSILFGNDCERTKHLDLVMLVTEVIAYSHCCMNPVI 300
 Db 301 yafvgerfrkylrhffhrlhmlhlgryipfipseklertssvspstaepelsivf 355
 QY 301 YAFVGERFRKYLRRHFFRHLHMLHGRYPFIPSEKLERTSVSSVSPSTAEPELSIVF 355

RESULT 5
 ID W03377 standard; Protein; 355 AA.

QY 202 RMTIFCLVPLVMAICYTGIIKTLRCPS-KKKYRAIRLIFVIMAVFFIFWTPYNVAIL 260
Db 257 lntfgef-fglncssnrlldqamqvtetlgtmthccinpiiyafvgekfrnyllvffqkh 315
QY 261 LSSYQSILFG-NDCERTKHLDLVNLVTEVIAYSHCCMNPIYAFVGERPKYLRHFFHRH 319
Db 316 iakrfckccsifqgeaperassvytrstgeqelsv 350
QY 320 LLMHLGRYIPFLPEKLERISSV-SPSTAEPELSI 353

Search completed: Tue Dec 8 13:15:18 1998
Job time : 59 secs.

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ch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 8 22:05:26 1998; MasPar time 2176.70 Seconds
Tabular output not generated. 1389.546 Million cell updates/sec

Title: >US-08-963-656-1

Description: (1-1689) from US08963656.seq

Perfect Score: 1688

N.A. Sequence: 1 ATCTCTTTTCCTGGCACCTC.....CCCTGCTTAATGAAGCTT 1689

Comp: TTAGGAAAAGGACCGTGGAG.....GGACGAATTAATTTTCGAA

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 2275036 seqs, 895388244 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-est55

Database: genbank-est107

5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13
10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17
14:gb_est18 15:gb_est19 16:gb_est20 17:gb_est21
18:gb_est22 19:gb_est23 20:gb_est24 21:gb_est25 22:gb_est26
23:gb_est27 24:gb_est28 25:gb_est29 26:gb_est30 27:gb_est31
28:gb_gss3 29:gb_gss4

Statistics: Mean 11.804; Variance 2.047; scale 5.765

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	204	12.1	450	20	W04836	0.00e+00
2	119	7.0	542	8	AA547303	1.85e-196
3	117	6.9	447	11	AA671573	6.05e-192
4	69	4.1	252	12	AA754459	4.23e-87
5	54	3.2	252	12	AA754459	1.18e-56
6	52	3.1	247	12	AA754458	9.65e-53
7	50	3.0	469	27	B84215	7.17e-49
8	48	2.8	247	12	AA754458	4.78e-45
9	39	2.3	2275	11	AF034173	1.59e-28
10	37	2.2	2275	11	AF034173	4.85e-25
11	36	2.1	456	25	AA354393	2.50e-23
12	35	2.1	553	26	FR0019847	1.22e-21
13	34	2.0	529	23	AA177828	5.66e-20

C	14	33	2.0	539	26	FR0019844	F.rubripes GSS sequenc	2.48e-18
C	15	33	2.0	602	7	AA511931	vg17f07.r1 Soares mous	2.48e-18
C	16	32	1.9	310	19	B70844	za73h08.s1 Homo sapien	1.02e-16
C	17	32	1.9	390	26	N33851	HS-1023-A2-F08-MR.abi	1.02e-16
C	18	32	1.9	507	12	AA795654	vs51h08.r1 Stratagene	1.43e-13
C	19	32	1.8	249	16	H29103	ym31f07.r1 Homo sapien	1.43e-13
C	20	30	1.8	380	25	AA354040	EST62304 Jurkat T-cell	1.43e-13
C	21	31	1.8	391	23	AA153412	mq66a06.r1 Soares 2NBM	3.95e-15
C	22	31	1.8	484	23	AA120018	mp93c11.r1 Soares 2NBM	3.95e-15
C	23	30	1.8	604	18	AA178926	EST222608 Normalized r	1.43e-13
C	24	31	1.8	639	12	AA816049	vr14h02.r1 Barstead mo	3.95e-15
C	25	31	1.8	723	22	AA1822270	mt83f08.r1 Soares mous	3.95e-15
C	26	29	1.7	128	16	H24894	yl13e08.s1 Homo sapien	4.79e-12
C	27	29	1.7	242	13	T25959	ATH352 HTCDL1 Homo sap	4.79e-12
C	28	29	1.7	251	8	AA94554	ne38h06.s1 NCI_CGAP-Co	4.79e-12
C	29	29	1.7	252	25	AA346471	EST52629 Fetal heart I	4.79e-12
C	30	29	1.7	354	15	AA954002	oo91a08.s1 NCI_CGAP-Ki	4.79e-12
C	31	29	1.7	366	15	AA955292	os27d07.s1 NCI_CGAP-Ki	4.79e-12
C	32	29	1.7	429	22	AA159773	zo80f07.r1 Stratagene	4.79e-12
C	33	29	1.7	450	21	W37302	zc09a11.s1 Soares para	4.79e-12
C	34	29	1.7	464	5	T89647	ye11h10.s1 Homo sapien	4.79e-12
C	35	29	1.7	465	17	AI097155	qb89b03.x1 Soares.feta	4.79e-12
C	36	29	1.7	475	11	AA679851	ac83f12.s1 Stratagene	4.79e-12
C	37	29	1.7	481	18	AA878538	oj19e07.s1 NCI_CGAP_Ki	4.79e-12
C	38	29	1.7	500	18	AI149461	qc78b10.x1 Soares.plac	4.79e-12
C	39	29	1.7	513	10	AA622285	no42906.s1 NCI_CGAP-Pr	4.79e-12
C	40	29	1.7	522	15	AI000789	oc02h07.s1 NCI_CGAP_GC	4.79e-12
C	41	29	1.7	530	14	AA848828	EST191589 Normalized r	4.79e-12
C	42	29	1.7	568	12	AA746256	ob08b11.s1 NCI_CGAP_Ki	4.79e-12
C	43	29	1.7	569	14	AA887979	nq95h08.s1 NCI_CGAP-Co	4.79e-12
C	44	29	1.7	586	26	FR0019937	F.rubripes GSS sequenc	4.79e-12
C	45	29	1.7	620	6	W87428	zh57e03.s1 Soares feta	4.79e-12

ALIGNMENTS

RESULT	1	W04836	450 bp	MRNA	EST	23-APR-1996
LOCUS		za81f05.r1 Soares fetal lung NDHL19W Homo sapiens cDNA clone 298977				
DEFINITION		5' similar to gb:D10925 C-C CHEMOKINE RECEPTOR TYPE 1 (HUMAN);				
		mrna sequence.				
ACCESSION		W04836				
NID		g1277557				
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				
		Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;				
REFERENCE		1 (bases 1 to 450)				
AUTHORS		Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.				
TITLE		The WashU-Merck EST Project				
JOURNAL		Unpublished (1995)				
COMMENT		Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL: contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: mob.REGA-ET High quality sequence stop: 402. Location/Qualifiers 1. .450 /organism="Homo sapiens" /note="Organ: lung; Vector: pT7f3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st				

3
 RESULT AA671573 447 bp mRNA EST 25-NOV-1997
 LOCUS V104901.r2 Soares mouse mammary gland NbMMG Mus musculus cDNA clone
 DEFINITION 963216 5' similar to TR:G1322040 G1322040 C-C CHEMOKINE RECEPTOR.
 ; mRNA sequence.
 ACCESSION AA671573
 NID G2643652
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 447)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Willson, R. and
 Waterston, R.
 TITLE The WashU-HMMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT

Contact: Marra M/Mouse EST Project
 WashU-HMMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:552008
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 397.

FEATURES

source
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 /strain="C57BL/6J"
 /note="Organ: mammary gland; Vector: pT73D-Pac
 (Pharmacia) with a modified polylinker; Site.1: Not I;
 Site.2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5',
 TGTTCACCAATCTGAGTGGGACGGCGCGGAATGTTTTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT73 vector.
 RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
 constructed and normalized by Bento Soares and M.Fatima
 Bonaldo."
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 /dev_stage="4 weeks"
 /lab_host="DH10B"
 BASE COUNT 104 a 102 c 92 g 149 t
 ORIGIN

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 Best Local Similarity 66.08; Pred. No. 6.05e-192;
 Matches 293; Conservative 0; Mismatches 146; Indels 5; Gaps 5;
 Db 5 TCACAGGCTCTATCATGTGGTTATTTGGTGAATCTCTTTCATATGCTCTCTGCACAA 64
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 QY 506 TCTCAGGTTTATACACAGGCTTTGACAGCAGATCTTTTCATATGCTCTGCACAA 565
 Db 65 TTGATAGGTACTTGGTATTGTCCATGCTGTGTTTGTCTTTAAAGTCAGACGGTCAACT 124
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 566 TCGACAGGTACCTGGCCATGTTCATGCTGTGTTTGGCTTCGACGCCGACGTGCACIT 625
 Db 125 TTGGGTGATAACAAGTGTAGTCACATTGGCGGCTGGCTGTGTTGGCTCTCTCCCGAAG 184

QY 626 TTGGTGTATCACCAGCATCGTCACCTGGCGGCTGGCAGTGTAGCAGCTCTCTCTGAAT 585
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 Db 185 TAATCTTTACCAGATCTCAGAAGAAGGTTTTCATATATACATGACAGTCTCTCAATTTCCAC 244
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 QY 686 TTATCTTCTATGAGACTGAAGAGTGTGTTTGAAGAGACTCTTTGCACTGCTCTTTACCCAG 745
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 Db 245 ACACCT-CAGTATCATTTCTGGAAGAGTTTCCAAACATTAAGATGTCATCTTGAGCCCTG 303
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 746 AGGATACAGTAT-ATAGCTGGAGGCAATTTCCACACTCTGAGAATGACCATCTGTGCTC 804
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 Db 304 ATCTCGCCCTTACTTGTCTATGCTCTCTACTCAGGAATTTCTCCACACCTCTGTTTCGC 363
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 Db 364 TGTAGGAATGAGAAGAAGCAGGCGGTGTGAGGCTCATCTTTGCCATCATGATTTGTC 423
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 QY 865 TGCCCCAGTAAAAA-AA-AGT-ACAAGGCCATCCGCTCATTTTGTCTCATCATGCGGGTG 921
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 Db 424 TACTTCTCTTCTGCACTCCCTAC 447
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 QY 922 TTTTTCATTTTCTGGACACCTTAC 945
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4
 RESULT AA754459 252 bp mRNA EST 20-JAN-1998
 LOCUS 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
 DEFINITION cDNA clone 97SN1787, mRNA sequence.
 ACCESSION AA754459
 NID G2801165
 KEYWORDS EST.
 SOURCE rice.
 ORGANISM Oryza sativa
 Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
 Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
 Poales; Poaceae; Oryza.
 1 (bases 1 to 252)
 Nahn, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R., Moon, E.P.,
 Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y.,
 Lee, M.C. and Eun, M.Y.
 Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
 Unpublished (1998)
 TITLE
 JOURNAL
 COMMENT

Contact: Eun M.Y.
 Department of Cytogenetics
 National Inst. of Agri. Sci. and Tech, RDA
 Suwon, Kyunggido, Korea
 Tel: 82 331 290 0301
 Fax: 82 331 290 0307
 Email: myeun@sun20.asti.re.kr
 Submitted by Baek Hie Nahn, Dept of Biological Science, Myongji
 University, Yongin, Korea. 449-728 bnhnm@bioserver.myongji.ac.kr
 Seq primer: M13 Reverse Primer.

FEATURES

source
 1..252
 /organism="Oryza sativa"
 /cultivar="Milyang23"
 /note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2:
 XhoI; Directional cDNA library inserted into lambda ZAPII
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 /lab_host="E. coli SOLR"
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 Best Local Similarity 13.8%; Pred. No. 4.23e-87;
 Matches 33; Conservative 125; Mismatches 76; Indels 5; Gaps 5;

SOURCE	ORGANISM
house mouse.	Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	
Mus.	
REFERENCE	
AUTHORS	
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.	
TITLE	The WashU-HMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	
Contact: Marra M/Mouse EST Project	
WashU-HMI Mouse EST Project	
Washington University School	
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	

```

tax: 314 200 1010
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:381203
Seq primer: -28M13 rev2 from AmerSham
High quality sequence stop: 494.
Location/Qualifiers
1. .529
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/strain="C57BL/6J"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCAATGAGGCGCGCGCTTTTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M.Fatima Bonaldo."
/db_xref="taxon:10090"
/clone="620379"
/clone_lib="Scares mouse 3mhw"

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/dev_stage="4 weeks"
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<1..>529
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BASE COUNT 110 a 168 c 107 g 144 t
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Matches 117; Conservative 0; Mismatches 65; Indels 3; Gaps 2;
Db 134 CAACCTGGCCATCGCAGATCTCCTTTCTGTGTGCACACTGCCATTTAGATCGCCTACCA 193
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QY 402 CAACCTGGCCATTCGGACCTGCTTCTCTCGTCACCCCTCCATTCCTGGATC--C-CTA 458
|||||
Db 194 TCTCAATGGCAACAACCTGGGTATTTGGCGAGGTCACTGCCGGATTCACCCAGGTTGTTTT 253
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QY 459 TGTCAAGGGGGCATAACTGGGTTTTTTGGCCATGGCATGTGTAAGCTCTCTCAGGGTTTTTA 518
|||||

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QY	519	TCACACAGGCTTGTCACGCGAGATCTTTTTCATAATCCTGCTGACAATCGACAGGTACCT	578
Db	314	GGCCA	318
QY	579	GGCCA	583
RESULT			14

[illegible]

(TM)

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ch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

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in on: Tue Dec 8 23:13:06 1998;. MasPar time 241.51 Seconds
951.505 Million cell updates/sec
bular output not generated.

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title:
description:
Accession:
RefSeq Score:
A. Sequence:
Comp:
>US-08-963-656-1
(1-1689) from US08963656.seq
1688
1 AATCTTTTCTGACACTC.....CCCTGCTTAATGAAAGCTT 1689
TTAGGAAGAAGCACCGTGGAG.....GGGACGAATTACTTTTCGAA

```

scoring table: TABLE default
Gap 6

match STD : Dbase 0; Query 0

188442 seqs, 68026449 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

database: n-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 9.514; Variance 5.518; scale 1.724

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description	Pred. No.
		Match	Length	DB			
1	1688	100.0	1689.23	T31334	CC-chemokine receptor	0.00e+00	
2	1688	100.0	1689.32	T58783	Human C-C chemokine r	0.00e+00	
3	1639	97.1	1315.34	T85162	Human chemokine recep	0.00e+00	
4	1637	97.0	5099.38	T93601	Human eosinophil eota	0.00e+00	
5	1116	66.1	1116.23	T31336	CC-chemokine receptor	0.00e+00	
6	1112	65.9	1193.23	T31335	CC-chemokine receptor	0.00e+00	
7	1030	61.0	1071.36	T75096	Human CCR3 chemokine	0.00e+00	
8	424	25.1	1065.33	T85154	Human MIP-1alpha/RANT	4.11e-281	
9	424	25.1	1495.11	Q62695	C-C chemokine recepto	4.11e-281	
10	424	25.1	2156.34	T90384	Human MIP-1 alpha/RAN	4.11e-281	
11	355	21.0	1544.34	T86839	CDNA encoding rat CC	1.24e-230	
12	225	13.3	1059.34	T85163	Macaque chemokine rec	2.47e-136	
13	222	13.2	1225.39	T75920	DNA encoding humanCC	3.54e-134	

222	13.2	1255	39	T76919	DNA encoding human CC	3.54e-13	
222	13.2	1434	25	T40402	Human G-protein chemo	3.54e-134	
222	13.2	1477	37	T90117	Human G-protein CCR5	3.54e-134	
222	13.2	3383	34	T85161	Human chemokine recep	3.54e-134	
222	13.2	1083	35	T96976	Human monocyte chemoa	1.43e-100	
175	10.4	1973	15	Q62928	Human monocyte chemoa	1.43e-100	
220	16.9	2232	15	Q96297	Human monocyte chemoa	2.61e-96	
220	16.9	90	792	37	T90116	CDNA for inactive hum	2.75e-84
222	15.2	90	1442	37	T90118	CDNA for inactive hum	2.75e-84
222	15.2	90	1557	39	T99542	Human chemokine recep	2.75e-84
223	7.3	1607	23	T32277	Chemokine receptor K5	5.55e-64	
223	7.3	1607	23	T32277	Chemokine receptor K5	5.55e-64	
225	7.6	4.5	1586	26	T44099	Human G-protein recep	5.47e-32
225	7.6	4.1	1900	11	Q61153	Partial coding sequen	2.18e-27
227	6.9	4.1	2058	11	Q61653	Putative seven transm	2.18e-27
228	6.9	4.1	2154	11	Q64125	Epstein barr virus in	2.18e-27
228	6.9	4.1	2154	11	Q64125	Putative seven transm	2.18e-27
330	6.5	3.9	2751	11	Q66164	Seven transmembrane r	8.68e-25
331	6.0	3.6	1162	11	Q66170	Seven transmembrane r	1.42e-21
332	6.0	3.6	2234	11	Q66167	Seven transmembrane r	1.42e-21
332	6.0	3.6	2234	11	Q66167	Seven transmembrane r	1.42e-21
344	5.3	3.1	1373	17	Q99951	Human dendritic cell	2.09e-18
344	5.3	3.1	1373	17	Q99951	Recombinant high affi	3.75e-17
336	5.1	3.0	1316	39	T99543	Human chemokine recep	6.57e-16
336	5.1	3.0	1547	40	V15419	Human macrophage/dend	6.57e-16
337	4.9	2.9	1200	5	Q30011	Sequence encoding a h	1.13e-14
338	4.9	2.9	1200	17	Q99949	Recombinant high affi	1.13e-14
339	4.8	2.8	1176	17	Q99950	Recombinant high affi	4.61e-14
40	4.8	2.8	1883	17	Q99006	Interleukin-8 recepto	4.61e-14
40	4.8	2.8	1933	5	Q29505	Interleukin-8 recepto	4.61e-14
42	4.4	2.6	1933	13	Q80520	Interleukin-8 recepto	4.61e-14
43	4.3	2.6	514	23	T35278	Chemokine receptor CD	1.22e-11
44	4.3	2.5	1373	5	Q90018	Sequence encoding a l	4.82e-11
44	4.3	2.5	1748	17	Q99008	Interleukin-8 recepto	4.82e-11

ALIGNMENTS

```

RESULT 1
ID T31334 standard; DNA; 1689 BP.
AC T31334;
DE 15-NOV-1996 (first entry)
DE CC-chemokine receptor 3 genomic DNA.
KW CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;
KW antinflammatory; eosinophil; ds.
OS Homo sapiens.
FH Key
FH cds
FT Location/Qualifiers
FT 181..1248
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FT 1007..1008
FT /*tag= b
FT variation
FT FT
FT FT
FT /*note= "CKR-3 genomic clone has GC at positions
FT 1007-1008, coding for threonine (ACG) at
FT position 276; a cDNA clone has GC at
FT these positions, coding for serine (AGC)"
FT misc_difference 1291
FT /*tag= c
FT /*note= "base n at position 1291 is not identified
FT in the specification"
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FT 25-JUL-1996.
FT 19-JAN-1996; U00608.
FT PF
FT PR 19-JAN-1995; US-375199.
FT PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
FT PA (CHIL-) CHILDRENS MEDICAL CENT.
FT (LEUK-) LEUKOSITE INC.
FT Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
FT Qln S;
FT WPI; 96-354528/35.
FT R-PSDB; W03376.
FT DR
FT PT Mammalian chemokine receptor-3 and related nucleic acids - useful
FT PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
PT Claim 1; Page 109; 153pp; English.
CC A genomic DNA clone (T31334) codes for a novel receptor (W03376),

```

CC designated Eos L2 or C-C chemokine receptor 3 (CCR-3), involved
 CC in leukocyte migration associated with inflammation. It was
 CC isolated from a human genomic library in EMBL3 SP7/17 vector by
 CC screening with a PCR fragment generated from eosinophil cDNA
 CC using degenerate primers (see also T31337-44). A CCR-3 cDNA
 CC clone (T31335) was also isolated, and a consensus sequence is
 CC given in T31336. The genomic and cDNA clones can be used for
 CC the prodn. of recombinant CCR-3 in host cells, or to design
 CC antisense sequences useful for treating inflammatory disease.
 SQ Sequence 1689 BP; 431 A; 416 C; 344 G; 497 T;

Query Match 100.0%; Score 1688; DB 23; Length 1689;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 1689; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Qy 61 GCTATCACATGTGCACTCTTTGTTGAGTACATGAATAAATCACTGGTGTGTTTACGAA 120
 Db 121 ggaatgattatgcttcattgtgggattgattttcttctctatcacagggagagtgaa 180
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 Db 181 atgacaacctcactagatatacagttgagaccttgggtaccacactctactatgatgacgtg 240
 Qy 181 ATGACAACCTCACTAGATACAGTTGAGACCTTGGTACCACATCTACTATGATGACGTG 240
 Db 241 ggctgctctgtaaaagctgatacagagacactgatggccagtttggccccctg 300
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 Qy 301 TACTCCCTGGTGTTCACGTGGGCTCTTGGGCAATGTGGTGGTGTGATGATCTCTATA 360
 Db 361 aaatcacaggaggtccgaattatgaccaacatctacgtctcaacctggccatttcggac 420
 Qy 361 AAATACAGAGGCTCCGAATATGACCAACATCATACCTGTCTCAACCTGGCCATTTGCGAC 420
 Db 421 ctgctcttctcgtcaaccttccatttggatccactatgtcaggggggataaactgggtt 480
 Qy 421 CTGCTCTTCCCTCGCACCTTCCATTTGGATCCACTATGTGACGGGGGCATATAACTGGGTT 480
 Db 481 ttggcctggcagtgtaagctcctctcagggttttatcacacagagcttgtacagcag 540
 Qy 481 TTTGGCCATGGCATGTGTAAGCTCTCTCAGGGTTTATACACAGAGCTGTGTACAGCGAG 540
 Db 541 atcttttccataactcctgctgacaatcgacaggttaccctggccattgtccatgctgttt 600
 Qy 541 ATCTTTTTCATAATCCTGTCTGACAAATCGACAGGTACCTGGCCATTGTCCATGCTGTT 600
 Db 601 gcccttgagcccgagctgtcaacttttgggtcactaccagacatcgtcaacctggggcctg 660
 Qy 601 GCCCTTGAGCCCGAGCTGTCACTTTTGGTGTCTATCACCAGCATCGTCACCTGGGGCTG 660
 Db 661 gcagtctagcagctcttctcctgaattctctctatgagactgaaggtgtttgaaag 720
 Qy 661 GCATGTAGCAGCTCTCTCTGAATTTATCTTCTATGAGACTGAAGAGTGTGTTGAAGAG 720
 Db 721 actcttgcagtgctcttaccagaggtacagtatatagctggaggtcatttccacact 780
 Qy 721 ACTCTTTGCACTGTCTTTACCCAGAGGATACAGTATATAGCTGGAGGCAITTCACACT 780
 Db 781 ctgagaatgacacattctctgctgttctcctctctgctgttattgagccatctgtacaca 840
 Qy 781 CTGAGAATGACACATCTTCTGCTCGTCTCCCTCTGCTGTATATGGCATCTGTGTACACA 840
 Db 841 ggaatcatcaaacgctgctgaggtgccagtaaaaaaagtaacagggccatccgctc 900
 Qy 841 GGAATCATCAAAACGCTGCTGAGGTGCCAGTAAAAAAGTAAAGGCCATCCGGCTC 900

Qy 841 GGAATCATCAAAACGCTGCTGAGGTGCCCGAGTAAAAAAGTAAAGGCCATCCGGCTC 900
 Db 901 attttgtcatatggtggtgttttcttcaatttttggacacctacataatgtgggtatcctt 960
 Qy 901 ATTTTGTCTATCATGCGGTGTGTTTTCATTTTGTGGACACCTTACAAATGTGGTATCCTT 960
 Db 961 ctcttctcatcaatccatcttatttggaaatgactgtgagcgaggaagatctcggac 1020
 Qy 961 CTCTCTTCTCATCAATCCATCTTATTGGAATGACTGTGAGCGGACGAAGCATCTGGAC 1020
 Db 1021 ctggtcatgctggtgacagaggtgacgctactcccactgtgctgcatgaacccggtgac 1080
 Qy 1021 CTGCTATGCTGTGACAGAGGTGATCGCTACTCTCCACTGCTGCTGATGAACCCGGTGATC 1080
 Db 1081 tagcctttgttggagagaggttccggaaagtacctcgccacttttccacagggcacttg 1140
 Qy 1081 TAGCGCTTTTGTGGAGAGAGGTTCCGGAAAGTACCTCGCCACTTCTTCCACAGGCCTTG 1140
 Db 1141 ctatgcacctggggagagatatcccatcttctcctctagtgagagactggaaagaccagc 1200
 Qy 1141 CTCATGCACCTGGGCAATACATCCCATTTCTTCCTAGTGAAGCTGGAAGAACCCAGC 1200
 Db 1201 tctgtctctccatccacagcagcgaggaactctctattgtgttttaggtagatgcagaa 1260
 Qy 1201 TCTGTCTCTCCATCCACAGCAGAGCCGGAACCTCTATTGTGTTTGGTGTAGTATGCAGAA 1260
 Db 1261 aattgctctaaaggaggaaggaacagagatnaagcaaacacattaaagccttccacactca 1320
 Qy 1261 AATTGCTTAAAGAGGAGGACCAAGGAGATNAAGCAAAACATTAAGCCTTCCACACTCA 1320
 Db 1321 cctctaaaaacagtccttcaaaccttccagtgcaaacactgaagcttcttaagacactgaaat 1380
 Qy 1321 CCTTAAACAGTCTCTCAAACTTCCAGTGAACACTGAAGCTTTAAGACACTGAAAT 1380
 Db 1381 atcacacagcagtagcagtagatgcatgtacccttaaggtcattaccacagggccagggct 1440
 Qy 1381 ATACACACAGCAGTAGCAGTAGATGATGATGTACCTTAGGTCTATTACACAGGCCAGGGCT 1440
 Db 1441 gggcagcgtactcatcatcaaaccttaaaagcagaggtttgcttctctctctctctctctct 1500
 Qy 1441 GGGCAGCGTACTCATCATCAACCTTAAAGAGCAGAGCTTGTCTCTCTCTCTCTCTCTCTCT 1500
 Db 1501 taactatatttttaatgcaccctgaatgttagatagatgtactatagcgcgtacacaaaggta 1560
 Qy 1501 TACTATATTTTAAATGCACCTGAATGTTAGATAGTTACTATATATGCTATATGCTATCAAAAAGGTA 1560
 Db 1561 aaacttttatatttatatacattacattacagcagctattataataaataaacatttca 1620
 Qy 1561 AAATTTTATATTTTATATACATTTAATTTCAGCCAGCTATTATATATAATAAATCAATTTTCA 1620
 Db 1621 cacaatacaataaagtttaactatttttcttaattgtgcttagtttcttccctgcttaat 1680
 Qy 1621 CACAATACATAAAGTTAACTATTATTTTCTTAATGTGCTAGTCTTCTTCCCTGCTTAAT 1680
 Db 1681 gaaaagcctt 1689
 Qy 1681 GAAAAGCTT 1689

RESULT 2
 ID T58783 standard; DNA; 1689 BP.
 AC T58783;
 DT 30-SEP-1997 (first entry)
 DE Human C-C chemokine receptor 3 DNA.
 KW Human; eotaxin; eosinophil; chemoattractant; stimulation;
 KW accumulation; attraction; chemotaxis; diagnosis; prevention;
 KW treatment; disease; inflammation; allergy; asthma; rhinitis;
 KW hypersensitivity; lung; pneumonia; Loeffler's; syndrome;
 KW interstitial; IiD; idiopathic pulmonary fibrosis;
 KW rheumatoid arthritis; systemic; lupus erythematosus; SLE;
 KW ankylosing spondylitis; scleritis; Sjorgen's; polymyositis;
 KW dermatomyositis; bowel; anaphylaxis; drug; penicillin;
 KW cephalosporin; insect sting; Crohn's; ulcerative colitis;

spondyloarthropathy; scleroderma; psoriasis; dermatosis; dermatitis; eczema; atopic; urticaria; necrotising; cutaneous; vasculitis; myositis; fascitis; multiple sclerosis; myasthenia gravis; juvenile onset diabetes; glomerulonephritis; autoimmune; thyroiditis; Bechet's; graft rejection; transplantation; allograft; graft versus host; cancer; leukocyte infiltration; reperfusion injury; atherosclerosis; haematologic malignancy; septic; endotoxic; shock; polymyositis; dermatomyositis; immunosuppression; immunodeficiency; AIDS; radiation therapy; chemotherapy; autoimmune; corticosteroid; Homo sapiens.

Location/Qualifiers
181..1248
Key cds
FT
FT
FT

W09700960-A1.
09-JAN-1997.
21-JUN-1996; U10723.
23-JUN-1995; US-494093.
PA (LEUK-) LEUKOSITE INC.
PI Mackay C., Newman W., Ponath PD., Qin S., Ringler DJ;
DR WPI: 97-087387/08.
DR P-PSDB: W10100.
PT New isolated human eotaxin gene - used to develop prods. for the
PT diagnosis and treatment of e.g. inflammation, allergies, auto-immune
PT disease, infections and tumours
PS Example 7; Page 97; 130pp; English.
CC The present sequence encodes human C-C chemokine receptor 3 (CRK3),
CC to which human eotaxin (hE), an eosinophil specific chemoattractant
CC capable of stimulating eosinophil accumulation and/or attracting
CC eosinophils (including chemotaxis), binds.
CC hE can be used to develop products for the diagnosis, prevention or
CC treatment of HE associated diseases or conditions. The products can
CC be used to treat inflammatory or allergic diseases and conditions,
CC including respiratory allergic diseases (e.g. asthma, allergic
CC rhinitis, hypersensitivity lung diseases or pneumonia),
CC eosinophilic pneumonias such as Loeffler's syndrome and chronic
CC eosinophilic pneumonia, interstitial lung diseases (ILD) such as
CC idiopathic pulmonary fibrosis or ILD associated with rheumatoid
CC arthritis, systemic lupus erythematosus (SLE), ankylosing
CC spondylitis, systemic sclerosis, Sjorgen's syndrome, polymyositis
CC or dermatomyositis), systemic anaphylaxis or hypersensitivity
CC responses, drug allergies (e.g. to penicillin and cephalosporins),
CC insect sting allergies, inflammatory bowel diseases (e.g. Crohn's
CC disease and ulcerative colitis), spondyloarthropathies,
CC scleroderma, psoriasis and inflammatory dermatoses (e.g.
CC dermatitis, eczema, atopic dermatitis, allergic contact dermatitis,
CC urticaria and necrotising, cutaneous and hypersensitivity
CC vasculitis), eosinophilic myositis and fascitis, multiple
CC sclerosis, SLE, myasthenia gravis, juvenile onset diabetes,
CC glomerulonephritis, autoimmune thyroiditis, Bechet's disease, graft
CC rejection (e.g. in transplantation) including allograft rejection or
CC graft versus host disease and cancers with leukocyte infiltration
CC of the skin or organs. The products can also be used to treat other
CC diseases or conditions requiring the inhibition of undesirable
CC inflammatory responses, including reperfusion injury.
CC atherosclerosis, certain haematologic malignancies, cytokine
CC induced toxicity (e.g. septic or endotoxic shock), polymyositis,
CC dermatomyositis, immunosuppression (e.g. in individuals with
CC immunodeficiency syndromes such as AIDS, undergoing radiation
CC therapy, chemotherapy, therapy for autoimmune disease or other drug
CC therapy, such as corticosteroid therapy, which causes
CC immunosuppression), immunosuppression due to (e.g. congenital)
CC deficiency (e.g. in eotaxin) or infectious diseases such as parasitic
CC diseases.
CC Degenerate primers based on the guinea pig eotaxin amino acid
CC sequence were used for the reverse transcriptase polymerase chain
CC reaction (RT-PCR) amplification of RNA isolated from inflamed,
CC eosinophilic lung tissue obtained from Balb/c mice sensitised to
CC ovalbumin. The amplification product was used as a probe to screen
CC a human genomic library in vector EMBL3 SP6/T7 to obtain the hE
CC gene.

SQ	Sequence	1689 BP;	431 A;	416 C;	344 G;	497 T;
	Query Match	100.0%;	Score 1688;	DB 32;	Length 1689;	
	Best Local Similarity	100.0%;	Pred. No. 0.00e+00;			
	Matches 1689;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Db	1 aatcctttcttcctgacccctctgataccttttgaattcatgtttaaagaatcccttaggct 60					
Qy	1 AATCCCTTTCTTCGGACCTCTGATATCCCTTTGAAATTCATGTAAAGAAATCCCTAGGCT 60					
Db	61 gctatcacatgtggcatctttgttgagtacatgaataaaatcaactgtgtgttttaccgaa 120					
Qy	61 GCTATCACATGTGGCATCTTTGTGTAGTACATGAATAAATCAACTGTGTGTGTTTACGAA 120					
Db	121 ggatgattatgcttcattgtgggattgtattttcttctctatcacagggagaaagtga 180					
Qy	121 GGATGATTATGCTTCATTGTGGGATTGTATTTTCTTCTTCTATCACAGGGAAGTGA 180					
Db	181 atgacaacctcactagatagacagttgagaccttgggtaccacatcctactatgatgacgtg 240					
Qy	181 ATGACAACCTCACTAGATACAGTTGAGACCTTTGGTACCACATCTCTACTATGATGACGTG 240					
Db	241 ggctgtctctgtgaaaaagctgataccagagcactgatggccagtttgtgcccgcgtg 300					
Qy	241 GGCTGTCTGTGTAAGAAAGCTGATACAGAGCACTGATGCCCAGTTTGTGCCCCGCTG 300					
Db	301 tactcctcctggttctcactgtgggaccttcttgggcaatgtggtggtgatgcctcata 360					
Qy	301 TACTCCTCGTGTGTACTGTGGGCTCTTTGGCAATGTGGTGTGTGATGATCCTCATA 360					
Db	361 aatatacagaggtccgaattatgacacacatcactcactcaacctgacatttccgac 420					
Qy	361 AATATACAGAGGCTCCGAATTAATGACCAACATCTACTGCTCAACCTGGCCATTTGGAG 420					
Db	421 ctgctcttcctcgtccaccttccattcttgatccactatgtcagggggagataaactgggtt 480					
Qy	421 CTGCTCTTCTCTGTCACCCCTTCCATTCTGGATCCACTATGTACAGGGGCATAACTGGGT 480					
Db	481 ttgggcattggcattgtgtaagctcctcctcagggttttatacacagagcttgtacagcag 540					
Qy	481 TTTGGCCATGGCATGTGTAAAGTCCCTCTCAGGGGTTTTATCACACAGGCTTGTACAGCGAG 540					
Db	541 atcttttataatacctcgtcgtgacaaatcgacagctactcgtgacatttccatcgtgttt 600					
Qy	541 ATCTTTTCAATAATCTGCTGACAAATCGACAGGACTACTGGCCATTGTCCATGTGTGTTT 600					
Db	601 gcccttgagcccgagctgtcacttttgggtcatcaccagcactgtcacctggggcctg 660					
Qy	601 GCCCTTCGAGCCCGGACTGTCACTTTTGGTGTCTATCACCAGCATCTGCACCTGGGGCCTG 660					
Db	661 gcagtgctagcagctcttcctgaaattattctctatgagactgaaagttgtttgaagag 720					
Qy	661 GCAGTGTCTAGCAGCTCTTCTCTGAATTTATCTTCTATGAGACTGAAGAGTTGTTTGAAGAG 720					
Db	721 actctttgagtgctctttaccagaggatatacagttatagctggagggaatttccacact 780					
Qy	721 ACTCTTTGAGTGCTCTTTTACCAGAGGATACAGTATATAGCTGGAGGGCATTTCCACACT 780					
Db	781 ctgagaatgaccattctctgtctctcctcctcgtctgttattggccactcgtctacaca 840					
Qy	781 CTGAGAATGACCATCTCTCTGCTCTGTTCTCCCTCTGCTGTTATGGCCATCTGCTACACA 840					
Db	841 ggaatcatcaaaacgtcgtgaggtgccccagtaaaaaaagataaaggccatccggctc 900					
Qy	841 GGAATCATCAAAACGCTGCTGAGGTGCCCCAGTAAAAAAGTACAAGGGCCATCCGGCTC 900					
Db	901 attttgtcatatggcgggtgttttctattttcttgacacacctacaaatgtggtatcctt 960					
Qy	901 ATTTTGTCTATCATGGCGGTGTTTTTCTATTTCTTGACACACCTTACAAATGTGGGTATCCTT 960					
Db	961 ctctcttcctatcaatcactcttatttggaaatgactgtgacgagcagacatctggac 1020					
Qy	961 CTCTCTCCTTCAATCCATCTTATTTTGGAAATGACTGTGAGCGGAGCAAGCATCTGGAC 1020					


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QY 720 GACTCTTTGCGAGTCTTTTACCAGAGGATACAGTATATAGCTGAGGACATTTCCACAC 779
Db 961 tctgagaatgaccattcttctgtctcttctccctctgctgttatggccatctgtctaac 1020
QY 780 TCTGGAATGACCATCTTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 839
Db 1021 aggaatcatcaaaacgctgctgaggtgccccagtaaaaaaagtaaaagccatccggt 1080
QY 840 AGGAATCATCAAAACGCTGCTGAGGTGCCCGAGTAAAAAAAGTCAAGGCCATCCGGCT 899
Db 1081 cattttgtcatatgaggtggttttttctattttcttgagaccctacataatgtggtatcct 1140
QY 900 CATTTTGTGTCATCATGCGGTGTTTTTCTATTTTCTGACACCCCTACAAATGTGGCTATCCT 959
Db 1141 tctcttctctatcaatcatctatttggaaatgactgtgagcgagcaagcatctga 1200
QY 960 TCTCTCTTCTTCAATCAATCATCTTATTGGAAATGACTGTGCGGACCAAGCATCTGGA 1019
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Db 1261 ctacgctttgttgagagaggttccggaagtacctgcgccacttcttccacaggaactt 1320
QY 1080 CTACGGCTTTGTTGGAGAGAGGTTCGGGAAGTACCTGCGCCACTTCTTCCACAGGCAT 1139
Db 1321 gctcatgcaacctggcgagatacattccattctctcttagtgagaaacttgaaagaaccag 1380
QY 1140 GCTCATGCACTGGGCGAGATACATCCATCTCTCTCTGAGAACTGGAAGAACCAAG 1199
Db 1381 ctctgctctccatccacagcagcggaactctattgtgttttaggtcagatgcag 1440
QY 1200 CTTCTGCTCTCCATCCACAGCAGCGCGGAACCTCTATTGTGTTTGGT-AGATGCAAG 1258
Db 1441 aaaaatgcttaaaagaggaagcaagagagatgaagcaaacacattaaagccttccacact 1500
QY 1259 AAAATTTGCTTAAGAGAGGACCAAGGAGATNAAGCAAAACATTAAGCTTCCACACT 1318
Db 1501 caactctaaaaagtccttcaaac-ttccagtgcaaacactgaagctcttgaagacactga 1559
QY 1319 CACCTCTAAACACAGTCTCTTCAAACCTTCCAGTGCACACTGAAGCTCTT-AAAGACACTGA 1377
Db 1560 aatatacacacagcagtagcagtagatgcattaccctaaaggtcattaccacagccag 1619
QY 1378 AATATACACACACAGTAGCAGTAGATGATGATGATGATGATGATGATGATGATGATG 1437
Db 1620 ggcctggcagcgtactcatcatcaatcaaacctcaaaagcagagcttgcctctctctaaaa 1679
QY 1438 G-CTGGGACGCTACTCATCATCAACC-TAAAAAGCAGAGCTTTGCTTCTCTCTAAAAA 1495
Db 1680 tgaattacctaattttaaagcactgaattgtagatagttactatgctgctgctcaaaaa 1739
QY 1496 TGAGTTACCTATATTTAATGCACTGATGATGATGATGATGATGATGATGATGATGAT 1555
Db 1740 agtataaaacttttattttatattacattacactcagcagctattatataataaaaaa 1799
QY 1556 AGTAAAAACCTTTTATTTTATTTATACATTAACCTCAGCCAGCTATT-ATATAAATAAACA 1614
Db 1800 ttttcacaaatacaataagtttaactatttttttctaagtgcctagttcttctccctg 1859
QY 1615 TTTTCACAAATACATAAGTTAACTATTTTATTTTCTTAATGTGCTAGTTCTTCTCCCTG 1674
Db 1860 cttaatgaaaagctt 1874
QY 1675 CTTAATGAAAAGCTT 1689
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RESULT 4

ID T93601 standard; cDNA; 5099 BP.
AC T93601;
DT 07-MAY-1998 (first entry)
DE Human eosinophil eotaxin receptor CC CKR3 encoding cDNA.
KW Eosinophil eotaxin receptor; CC CKR3; human; treatment; dermatitis;

KW atopic condition; allergic rhinitis; conjunctivitis; bronchial asthma;
KW beta-chemokine receptor; viral infection; ss.
OS Homo sapiens.
FH Key
FT misc_feature Location/Qualifiers
FT 1..3586
FT /*tag= a
FT /*note= "5' genomic DNA flanking sequence"
FT 3587..4654
FT /*tag= b
FT /*product= "human eosinophil eotaxin receptor"
FT 4655..5099
FT /*tag= c
FT /*note= "terminator region"
PN WO9741154-A1.
PD 06-NOV-1997.
PF 24-APR-1997; U065568.
PR 17-JAN-1997; GB-000894.
PR 26-APR-1996; US-016158.
PR 26-APR-1996; US-017113.
PA (MERI) MERCK & CO INC.
PI Daugherty BL, Demartino JA, Siciliano SJ, Springer MS;
DR WPI: 97-549685/50.
DR P-PSDB; W31850.
PT New isolated human eosinophil eotaxin receptor - used to develop
PT products for treating and preventing atopic conditions e.g. allergic
PT rhinitis, dermatitis, conjunctivitis and bronchial asthma
PS Claims 12, 13, 14; Pages 16-20; 51pp; English.
CC This cDNA encodes a human eosinophil eotaxin receptor. This 5099 base
CC pair sequence comprises a 1065 base pair open reading frame encoding a
CC 355 amino acid eosinophil eotaxin receptor protein, flanked by a 5',
CC genomic DNA sequence and a 3' terminator region. This novel eosinophil
CC eotaxin receptor is a human beta-chemokine receptor designated CC CKR3.
CC Agents which bind to this eosinophil eotaxin receptor can be used for
CC the treatment and prevention of atopic conditions such as allergic
CC rhinitis, dermatitis, conjunctivitis and bronchial asthma. Agents which
CC block this eosinophil eotaxin receptor can be used to prevent viral
CC infection in healthy individuals and slow or halt viral progression
CC in infected patients.
SQ Sequence 5099 BP; 1388 A; 1171 C; 1013 G; 1527 T;

Query Match 97.0%; Score 1637; DB 38; Length 5099;
Best Local Similarity 99.3%; Pred. No. 0.00e+00;
Matches 1683; Conservative 0; Mismatches 5; Indels 7; Gaps 7;
Db 3406 aatctctctctcggcactctgatatgccttttgaattcatgtttaagaatccctaggc 3465
QY 1 AATCTTTTCTCTGGCACCTCTGATAT-CCTTTTGAATTCATGTTAAAGAAATCCCTAGGC 59
Db 3466 tgctatcacatgtgcactcttctgttgagtcacatgaataaatacaactggtgttttaaga 3525
QY 60 TGCTATCATGTGGCACTCTTTGTTGAGTACATGAATAAATCAACTGGTGTGTTTACGA 119
Db 3526 aggatgattatcttcattctgtgggattgtattttctctctcttatcacaggagagtgga 3585
QY 120 AGGATGATTATCTTCATTGTGGGATTGATTTTCTTCTTATCACAGGAGAGTGA 179
Db 3586 aatgacaacctcactagatcacagttgagacctttgttaccacatcactactatgatgaagt 3645
QY 180 AATGACAACCTCCTAGATACAGTTGAGACCTTTGGTACCACATCCTACTATGATGACGT 239
Db 3645 gggcctgctctgaaaaagctgataccagacactgatgcccagatttgtgtcccccgct 3705
QY 240 GGGCCTGCTCTGTGAAAAAGCTGATACCAGACACTGATGGCCCAAGTTTGTGCCCCGCT 299
Db 3706 gtactccctggtgttcactgtggcctcttgggcaatgtggtggtggtgatatcctcat 3765
QY 300 GTACTCCCTGGTGTTCACGTGGGCTCTTGGGCAATGGTGGGTGATGATCTCTAT 359
Db 3766 aaaaatacaggaggtcccgaaattatgaccaacaatctacctgtctcaacctggtccatttcgga 3825
QY 360 AAAATACAGAGGCTCCGAATTTATGACCAACATCTACCTGCTCAACCTGGCCCATTTCCGA 419
Db 3825 cctgctctctctcgtcaacccttccattcttctggtatccactatgtcagggggcacaactgggt 3885

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QY 420 CTGCTCTCTCCGTCACCCCTTCCATCTCTGGATCCATATGTCAGGGGCAATACTGGGT 479
Db 3886 ttttgccatggtatgtgaagctctctcagcgggtttttatcacacagcgttgtagcaga 3945
QY 480 TTTTGGCCATGGCATGTGTAAGCTCCTCTCAGGGTTTATCACACAGGCTTGACAGGA 539
Db 3946 gatctttttcaatactctctgacaaatcagacaggttacctgceattgtccatgtgtgtt 4005
QY 540 GATCTTTTTCATATPCTTGCCTGACAATCGACAGGTACCTGGCCATTGTCCATGCTGTGT 599
Db 4006 tgccttcagccggagctgtcaacttttgggtgtcataccagcagctgtcacctggggcct 4065
QY 600 TGCCCTTCAGCCCGGACTGTCACTTTTGGTGTCTATCACCAGCATGCTCACCTGGGGCCT 659
Db 4066 ggcagtgtagcagctctctcgaatttatctctatgagactgaagagttgtttgaaga 4125
QY 660 GGCAGTGTAGCAGCTCTCTGTAATTTATCTCTATGAGACTGAAGAGTTGTTTGAAGA 719
Db 4126 gactctttgagtgctctttaccagagagatacagtatatagctggaggcaatttccacac 4185
QY 720 GACTCTTTTGCAGTGTCTTTTACCAGAGGATACAGTATATAGCTGGAGGCATTTCCACAC 779
Db 4186 tctgagaatgaccatctctctcgtctctcctctcgtctgttatggccatctgctacac 4245
QY 780 TCTGAGAAATGACCATCTCTCTGCTCTGCTTCTCCCTGCTGTTATGGCCATCTGCTACAC 839
Db 4246 aggaatcatcaaaacgctgtcggagtgccccagtaaaaaaagtacaggccatccggct 4305
QY 840 AGGAATCATCAAAAGCTGTCTGAGGTGCCCGCAGTAAAAAAGTACAAAGGCCATCCGGCT 899
Db 4306 catttttgtcatatggtgggtgttttttcaattttctggacacccctacaatgtggtatcct 4365
QY 900 CATTTTGTCTATCATGCGCGGTGTTTTTCATTTTCTGGACACCCCTACAAATGTGGTATCCT 959
Db 4366 tctcttctctatcaatccatctatttggaatgactgtgagcggagcaagcatctgga 4425
QY 960 TCTCTTCTCTATCAATCCATCTTATTGGAATGACTGTGAGCGGAGCAATCTGGA 1019
Db 4426 cctggtcatgtgtgacagaggtgatgcctactcccactgtcgtacatgaacccgggtgat 4485
QY 1020 CTGTGTATCTGTGTGACAGAGGTGATCGCCTACTTCCACTGCTGTCATGAACCCGGTGAT 1079
Db 4486 ctacgctttttgagagaggttccggaagtaactcgtgcgaacttcttccacagcactt 4545
QY 1080 CTACGCCCTTTTGGAGAGAGGTTCCGGAAGTACTGTGCGCACTTCTTCCACAGGCACTT 1139
Db 4546 gctcatgacctgggcagatcacatccatctctccttagtgagagactggaagaaacacag 4605
QY 1140 CTTATGACCTTGGCAGATACATCCCATCTCTTCTAGTGAGAGCTGGAAAGAACACAG 1199
Db 4606 ctctgtctctccatccacagcagagcgggaactctctattgttttaggtcagatgcag 4665
QY 1200 CTCTGTCTCTCCATCCACAGCAGAGCGGAACTCTCTATTGTGTTTAGGT-AGATGCAG 1258
Db 4666 aaaattgcttaagagaggaagaccaaagagatgaagcaaacacatttaagccttccacact 4725
QY 1259 AAAAATTGCTTAAGAGGAAGACCAAGAGATNAAGCAAAACACATTAAAGCCTTCCACACT 1318
Db 4726 cactctaaaaacagctcttcaaac-ttccagtgaacactgaactcttgaagacactga 4784
QY 1319 CACCTCTAAAACAGTCTTCAAACTTCCAGTGAACACTGAAGCTCTT-AAAGACACTGA 1377
Db 4785 aatacacacagcagtagcagtagatgcatgtacccttaaggtcattaccacagggccagg 4844
QY 1378 AATATACACACAGCAGTAGCAGTAGATGATGATACCCCTAAGGTATATACACAGGCCAGG 1437
Db 4845 ggcctggcagcgtactactatacaacccttaaaagcagagcttttgcctctctctctaaaa 4904
QY 1438 G-CTGGGAGCGGTACTCATCATCAACC-TAAAAAGCAGAGCTTTGCTTCTCTCTAAAA 1495
Db 4905 tgagtacctacattttaaagcactgaatgttagatgttactatgtatgctgcgtcacaaa 4964
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QY 1496 TGAGTTACCTATATTTTAAATGCACCTGAATGTTAGATAGTTACTATATGCGCTACAAA 1555
Db 4965 agtataaactttttatatatttatataacttaacttcagcagctatttgatataaaaca 5024
QY 1556 AGGTAAACATTTTATATTTTATACATTAACCTCAGCCAGCTATT-ATATAAATAAACA 1614
Db 5025 ttttcacacaatacaataaagtttaactattttatttttaataatgctagttcttccctg 5084
QY 1615 TTTTTCACACAAATCAATAAGTTAACTATTTTATTTTCTAAATGCGCTAGTTCTTCCCTG 1674
Db 5085 cttaaatgaaaagctt 5099
QY 1675 CTTAATGAAAAGCTT 1689

RESULT 5
ID T31336 standard; DNA; 1116 BP.
AC T31336;
DT 13-NOV-1996 (first entry)
DE CC-chemokine receptor 3 consensus DNA sequence.
KW CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;
KW antiinflammatory; eosinophil; ds.
OS Homo sapiens.
PN W0962371-A2.
PD 23-JUL-1996.
PF 19-JAN-1996; U00608.
PR 19-JAN-1995; US-375199.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (LEUK-) LEUKOSITE INC.
PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
PI Qin S;
PI WPI; 96-354528/35.
DR P-PSDB; W03378.
DT Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
PS Claim 1; Page 114-115; 153pp; English.
CC A consensus DNA sequence (T31336) codes for a novel human receptor
CC (W03378), designated Eos L2 or C-C chemokine receptor 2 (CKR-3).
CC It was deduced by comparing a genomic clone (T31334) and a cDNA
CC clone (T31335) coding for CKR-3 proteins (W03376 and W03377) having
CC slightly different sequences. Initial sequence information revealed
CC 2 regions in which the cDNA sequence appeared to be shifted in
CC frame, resulting in 2 sets of 4 contiguous amino acid differences
CC in the predicted proteins. Further sequence analysis revealed only
CC a single difference between the 2 open reading frames, the genomic
CC clone coding for threonine at position 276 and the cDNA clone for
CC serine.
SQ Sequence 1116 BP; 246 A; 286 C; 257 G; 306 T;

Query Match. 66.1%; Score 1116; DB 23; Length 1116;
Best Local Similarity 98.1%; Pred. No. 0.00e+00;
Matches 1095; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

Db 1 cagggagaagtgaatgacaaactcactcactgtagacagctttgggtaccacatcct 60
QY 167 CAGGGAGAAGTGAATGACAACTCCTACTAGATACAGTTGAGACCTTTGGTACCACATCCT 226
Db 61 actatgatgacgtgggcctcctctctgtgaaaaaagctgtataccagagactgatggccagt 120
QY 227 ACTATGATGACGTGGGCGCTCTCTGTGAAAAGCTGTATACAGAGCACTGATGGCCAGT 286
Db 121 ttgtgccccgcgtactcctcctggtgtcactgtggcctcttgggcaatgtggtgtg 180
QY 287 TTGTGCCCCCGCTGTACTCCTCTGGTGTCTACTGTGGCCCTTTGGGCAATGTGGTGGTG 346
Db 181 tgatgatctctataaaatacacagaggctccgaattatgaccaacatctacctgctcaacc 240
QY 347 TGATGATCTCTATAAATAATACAGGAGGCTCGGAATTATGACCAACATCTACCTGCTCAACC 406
Db 241 tggccatttcggagcgtctctcctgctcactccttcattctgattccactatgtcagg 300
|||||
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QY 407 TGGCCATTTCGGACCTGCTCTCTCTCGTCACACCTTCCATTTCTGGATCCACTATGTCAGGG 466
Db 301 ggcataactgggttttggccatgcatgtgaaactctctcaggggtttttatcacag 360
QY 467 GGCATAACTGGGTTTTTGGCCATGCACTGTGAAGCTCTCTCAGGGTTTTATCACACAG 526
Db 361 gctgtacagcagatctttttcataactctgctgacaatcagacaggtacctggccattg 420
QY 527 GCTGTACAGCCAGATCTTTTCATATCTCTGCTGACATCCAGAGTACCTGGCCATTG 586
Db 421 tccatgctgtgttgcccttcgagcccgactgctcaacttttgggttcacaccagcatcg 480
QY 587 TCCATGCTGTGTTTGCCTTCGAGCCGAGCTGTACATTTTGGTTCATCACCAGCATCG 646
Db 481 tcaactgggctggcagctgtagagctcttccgaatttatcttatgagacgaag 540
QY 647 TCACCTGGGGCTGGCAGTGTAGCAGCTCTTCCCTGAATTTATCTATGATGAGCTGAAG 706
Db 541 agttgttgaagactmttttcagtgctctttaccagagatcacagtatatagctgga 600
QY 707 AGTTGTTGAAGACTCTTTCGAGTGTCTTTACCAGAGATACAGTATATAGCTGGA 766
Db 601 gssattccacactctgagaatgacatctctgtctctctctctctctctctctctctctg 660
QY 767 GGCATTTCCACACTCTGAGAATGACATCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 826
Db 661 ccactctcacacaggaatcataaagcctgctgaggtgccccagtaaaaaaagtaca 720
QY 827 CCATCTGCTACACAGGAATCATCAAAACCTGCTGAGGTGCCCCAGTAAAAAAGTACA 886
Db 721 aggcaccccgctcattttgtcactcatgctggcggtgtttttcatttcttgacacccctaca 780
QY 887 AGCCATCCGGCTCAATTTTGTCTCATCATGCGCGGTGTTTTTCATTTCTGGACACCTTACA 946
Db 781 atgtggctatcctctctctctctctctctctctctctctctctctctctctctctctct 840
QY 947 ATGTGGCTATCTCTCTCTCTCTATCAATCCATCTATTTTGGAAATGACTGTGAGCGGA 1006
Db 841 mgarsmwykgaacctgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 900
QY 1007 CGAAGCATCTGACCTGGTGTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1066
Db 901 tgaacccggtgctacgccttctgttgagagaggttccggaagtacctgcccacttst 960
QY 1067 TGAACCCGGTGATCTACGCGCTTTGTGTGAGAGAGGTTCGGAAGTACCTTCCGCCACTCT 1126
Db 961 tccacagggcactgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 1020
QY 1127 TCCACAGGCACCTTGCTCATGCACTGGGCAGATACATCCATCTCTCTCTCTCTCTCTCT 1186
Db 1021 tggaaagaccgctgctgctctctctccatccacagcagagcgcgaactctctattgtgttt 1080
QY 1187 TGGAAAGAACCAAGCTGTCTCTCTCTCATCCACAGCAGAGCGGAACCTCTCTATTGTGTTT 1246
Db 1081 agtgatgacacaaaattccctaaagagagagacc 1116
QY 1247 AGGTAGATGCAAAAATTCCTTAAGAGGAGGACC 1282
```

RESULT 6

```
ID T31335 standard; cDNA; 1193 BP.
AC T31335;
DT 15-NOV-1996 (first entry)
DE CC-chemokine receptor 3 cDNA clone.
KW CC-chemokine receptor 3; CXR-3; Eos-L2; inhibitor; antisense;
KW antiinflammatory; eosinophil; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 92..1159
FT variation 918..919
FT /tag= a
FT /tag= b
FT /note= "CXR-3 cDNA clone has GC at positions
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FT 918-919, coding for serine (AGC) at
FT position 276; a genomic clone has CG at
FT these positions, coding for threonine
FT (AGC)."
PN WO9622371-A2.
PD 25-JUL-1996.
PR 19-JAN-1996; US-375199.
PF 19-JAN-1995; US-375199.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (LEUK-) LEUKOSITE INC.
PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
PI Qin S;
DR WPI: 96-354528/35.
DR P-PSDB; W03377.
DR Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
PS Claim 1; Page 111-113; 153pp; English.
CC A genomic DNA clone (T31335) codes for a novel receptor (W03377),
CC designated Eos L2 or C-C chemokine receptor 3 (CXR-3), involved
CC in leukocyte migration associated with inflammation. It was
CC isolated from a human library constructed from eosinophils obtd.
CC from a patient with hyper-eosinophilic syndrome using a probe
CC (p4 cDNA) encoding the MIP-lalpha/RANTES receptor. A CXR-3
CC genomic clone (T31334) was also isolated, and a consensus sequence
CC is given in T31336. The cDNA and genomic clones can be used for
CC the prodn. of recombinant CXR-3 in host cells, or to design
CC antisense sequences useful for treating inflammatory disease.
SQ Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T;
```

Query Match 65.9%; Score 1112; DB 23; Length 1193;

Best Local Similarity 99.8%; Pred. No. 0.008+00;

Matches 1114; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Db 78 caggagagaagtgaatgacaacctcactagatagacagcttgagacacctttgtaccacatcct 137
QY 167 CAGGAGAGAGTGAATGACACACCTCCTACTAGATACAGTTGAGACCTTTGGTACCACATCCT 226
Db 138 actatgtagcgtggcgctcctctgtgaaaaagctgtaccagagcactgtatggccacgt 197
QY 227 ACTATGATGACGTGGCGCTGCTCTGTGAAAAAGCTGTATACCAGAGCACTGATGGCCCACT 286
Db 198 ttgtgccccgcgtgactccctcctgtgttcactgtggcctcttgggcaaatgtgtgtgtg 257
QY 287 TTGTGCCCCCGCTGTACTCCCTGCTGTGTTCACTGTGGGCTCTTGGGCAATGTGTGTGTGG 346
Db 258 tgatgactctataaaatcacaggaggtccgaattatgaccaacatctacctgctccaacc 317
QY 347 TGATGATCTCTATAAAATACAGGAGGCTCCGAATATGACCAACATCTACCTGTCTCAACC 406
Db 318 tggccatttcggacgtgctctctcctcgtcacccctccattcttgatccactatgttcagg 377
QY 407 TGGCCATTTTCGACCTGCTCTTCTCTCGTCACTTCCATTTCCATTCGGATCCACATGTCAGG 466
Db 378 ggcataactgggttttggccatggcagctgtgtaagctcctctcagggtttttatcacag 437
QY 467 GGCATAACTGGGTTTTTGGCCATGGCATGTGTAAAGCTCTCTCAGGGTTTTATCACACAG 526
Db 438 gctgtacagcagagatctttttcataatcctcgtgacacgaatcagcaggtacctggccattg 497
QY 527 GCTTGTACAGCGAGATCTTTTTCATATCTCTGCTGACAAATGACAGGTACCTTGGCCATTG 586
Db 498 tccatgctgtgtttggcccttcgagcccgactgtcacttttgggtgtcatccaccagcatcg 557
QY 587 TCCATGCTGTGTTTGGCCCTTCGAGCCGAGACTGTCTACATTTTGGTGTCTATCACCACATCG 646
Db 558 tcaactgggctggcagctgtagcagctctctctctctctctctctctctctctctctctga 617
QY 647 TCACCTGGGGCTGGCAGTGTAGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 706
Db 618 agtttttgaagagactcttttgcagctctctttaccagagagatacagtatatactgga 677
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QY 1198 AGCTCTGCTCTCCATCCACAGACAGCCGGAACCTCTCTATTGTGTTTAG 1248

RESULTS

RESUL	8
ID	T86154 standard; cDNA; 1065 BP.

AC 196154; 1997 (first entry)
AD Human MIP-1alpha/RANTES receptor protein coding sequence.
DE
DI Human MIP-1 alpha/RANTES receptor; osteoporosis; pCCR; digestive ulcer;
KW macrophage inflammatory protein 1 alpha; diabetes; central disease;
KW regulated on activation, normal T cell expressed and secreted; allergy;
KW affinity compound; expression vector; CHO cell; viral disease;
KW infectious disease; tumour; hyperlipidaemia; hypercholesterolaemia; ss
OS Homo sapiens.
PN J09176048-A.
PN
PN 08-JUL-1997. 342130.
PN 28-DEC-1995; 342130.
PA (TAKE) TAKEDA CHEM IND LTD.
PA WPI: 97-399449/37.
DR P-PSDB: W25751.
DR
DR
PT Preparation of human MIP-1-alpha/RANTES receptor protein - used in
PT the treatment of viral diseases, tumours, allergy, diabetes
PT osteoporosis etc.
PS Claim 6; Page 15; 19pp: Japanese.
PS This sequence encodes human MIP-1 alpha/RANTES receptor (macrophage
CC inflammatory protein 1 alpha)/regulated on activation, normal T cell
CC expressed and secreted). The human MIP-1 alpha/RANTES receptor protein
CC may be used in a method for the screening of human MIP-1 alpha/RANTES
CC receptor affinity compounds. The MIP-1 alpha/RANTES receptor coding
CC sequence may be included in an expression vector, preferably pCCR, and
CC used to transform a CHO cell for use in the same method. The receptor
CC protein can provide a preventive and treating agent for viral diseases,
CC infectious diseases, tumours, allergy, diabetes, central diseases,
CC hyperlipidaemia, hypercholesterolaemia, osteoporosis, digestive ulcers,
CC etc.
SQ Sequence 1065 BP: 228 A: 284 C: 253 G: 300 T:

Query Match 25.1%: Score 424: DB 33: Length 1065:

Best Local Similarity 71.9%; Pred. No. 4.11e-281;

Matches	695;	Conservative	0;	Mismatches	271;	Indels	0;	Gaps	0;
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Db 99 ggcccaactgctgccccctctgtactccttggtattgtcatatggcctggttgaaacat 158
||||| | ||||||| ||||||| || ||||||| || ||||||| || ||||||| ||
279 GGCCACAGTTGTGCCCCCGGTGTACTCCCTGCTGTTCTACTGTGGGCCCTTGTGGCAATGT 338

Db 159 cctggtggtcctggtccttqtccaatacaagaggtctaaaaaacatgaccagcatctacct 218

QY 339 GGTGGTGATGATCCTCATAAAATACAGGAGGCTCCGAATTATGACCAACATCTACCT 398

Db 219 cctgaacctgqccatttctgacctgctctcctgattcacgccttcccttctgqatcgaacta 278

QY 399 GCTCAACCTGGCCATTTCGGACCTGCTCTTCCTCGTCACCCCTTCCATTCTGGATCCACTA 458

Db 279 caaqttaaaggatgaactgaatttttgaatgaccatgtgtaaagatcctctctggaattta 338

QY 459 TGTCAGGGGGCATAACTGGGTTTTTGGCCATGGCATGTGTAAAGCTCCTCTCAGGGTTTA 518

Db 339 ttacacagagctgtacacgcgagatctttttcatcatcctgctgacgattgacaggtacct 398

519 TCACACAGGCTTGTA CAGCGAGATCTTTTTCATTAATCCTGCTGACAAATCGACAGGTACCT 578

Db 399 qaccatcgtccacgcccgtgttttgcccttgaggacacgaccgtcaccttttggtgtcatcac 458

579 GGCCATTGTCCATGCTGTGTGTTGCCCTTCGAGCCCCGGACTGTCACCTTTGGTGTCATCAC 638

Db 459 cagcatcatatttggggccctggccatcttggccttccatgccaggcttatacttttccaa 518

OY 639 CAGCATCGTCACCTGGGGCTGGCAGTGCTAGCAGCTCTTCCTGAATTATCTTCTATGA 698

Db 519 gaccgaatgggaattcactcaccacacctgcagccttcactttcctcacgaaagcctacg 578

Qy	699	GACTGAAGACTGTTTGAAGAGACTCTTTGACGTGCTCTTTTACCAGAGGATACAGTATA	758
Db	579	agagtggaaagctgtttcaggcctctgaaactgaacctctttggcctggtaattgcccctttgtt	638
Qy	759	TAGCTGGAGGCAITTTCCACACTCTGAGAAATGACCATCTTCTGCTCGTCTCCCTCTGCT	818
Db	639	ggteatgatcatctgtctacacaggggattataaagattctgtctaagacgacccaaatgaa	698
Qy	819	CGTTATGGCCATCTGCTACACAGGAATCATAAAGCGTCTGAGGTGCCCAGTAAAAA	878
Db	699	gaaatccaaagctgtccgtttgatttttttcacatgacatctttttctctcttttggac	758
Qy	879	AAAGTACAAGGCCATCCGGCTCAATTTTGTCAFCATGCGGGTGTTTTTTCATTTCTGGAC	938
Db	759	ccctacaatttgactatactattctctgttttccaagactcctgttccaccatgagtg	818
Qy	939	ACCTTACAATGTGGCTATCCTTCTCTCTTCCATATCAATCCATCTTATTTGGGAATGACTG	998
Db	819	tgagcagagcagacatttgagacctgctgtgcaagtgcaggaggtgatcgctcacacgca	878
Qy	999	TGACGGGACCAAGCATCTGGACCTGTCATGCTGGTGACAGAGGTGATCGCCTACTCCCA	1058
Db	879	ctgctgtgtcaaccagtgatctacagcctctgttggtagaggttcggaaagtacctgcg	938
Qy	1059	CTGTGTGATGAACCCGGTGATCTACGCCCTTTGTTGGAGAGAGGTTCCGGAAGTACCTGCG	1118
Db	939	gcagttttccacaggcgtgtgagctgtgcaactggtaaataggctcccccttctctcgt	998
Qy	1119	CCACTTCTTCCACAGGCATTTGCTATGACCTGGGCAGATACATCCCATTCTTCCCTAG	1178
Db	999	ggacaggctggagagggtcagctccacatctcctccacaggggagcatgaaactcttcgc	1058
Qy	1179	TGAGAACTGGGAAGAACCACTCTGTCTCTCCATCCACAGCAGACCGGAACTCTCTAT	1238
Db	1059	tggggtt	1064
Qy	1239	TGTGTT	1244

RESULT

RESOLUTION 3
ID Q62695 standard; DNA; 1495 BP.

AC Q62695;

DE C-C chemokine receptor DNA.
KW C-C CKR-1; cytokine; inflammation; ds
OS Homo sapiens.

PN W09411304-A.
PD 26-MAY-1994.

PF: 04-NOV-1993; UI0672.
PR 10-NOV-1992: US-97402

PA (GETH) GENENTECH INC.
PI Horuk R. Neote K. Sch

DR WP1; 94-183505/22.
DR P-PSDB: R52749.

PT

PS cytokine-mediated disorders
Claim 17: Fig 9: 90pp: English

CC The sequence is that of the C-C ch
CC isolated by PCR from PMA treated H
CC

CC sequence was designed to correspond
CC transmembrane regions of known cytochrome

CC be used in therapeutic or diagnostic
CC other cytokine mediated disorders

SQ sequence 1495 BP; 348 A; 389 C;

Query Match	25.18; Score 424; D
Best [local] similarity	71.98; pred NC 41

Matches 695; Conservative 0; Mismatches 0;

bb 99 gcccactgctgccccctctgtactccttggatatctgc

QY 279 GCCCAGTTTGTGCCCCCCCCGCTGTA

Db	159	ctctgggtggctctggttctctgtgcaatatcaagagggtctaaataaacatgaccagcatctacct	218
Qy	339	GGTGGGTGGTATGATCCTCATAAATACAGGAGGCTCGGAATTATGACCAACATCTACCT	398
Db	219	cttgaacctggccatttctgacctgctctctctgttaacgcttccctctctggatcgacta	278
Qy	399	GCTCAACCTGGCCATTTCGGACCTGCTCTCTCTGTCGACCCCTTCATTTCTGGATCCCACTA	458
Db	279	caagttgaaggaatgactgggttttttgggtatgccatgtgtaagatccctctctgggtttta	338
Qy	459	TGTCAGGGGGCATAACTGGGTTTTGGCCATGGCATGTGAAGCTCCTCTCAGGGTTTTA	518
Db	339	ttacacagcctgttacagcgagatctttttcatcatctctgctgacgattgcaggtacct	398
Qy	519	TCACACAGGCTTGTACAGCGAGATCTTTTTCATATCCTGTGCAATCGACAGGTACCT	578
Db	399	ggccatgctccacgcgctgtttgcttgcgggcaagcgacctcaacttttgggtgctcatc	458
Qy	579	GGCCATTGTCCATGCTGTGTTTGGCCCTTCGAGCCCGGACTGTCACATTTGGTGTCACTAC	638
Db	459	cagcatcatcatttgggcccctggccatcttggcttccatgcccaggcttatactttccaa	518
Qy	639	CAGCATCGTACCTGGGGGCTGGCAGTGTACGACGCTCTCTCTGAATTTATCTTCTATGA	698
Db	519	gacccaatgggaattcaactcaccacacctgcagccttcactttctctcacgaagcctacg	578
Qy	699	GACTGAAGAGTGGTTTGANAGACACTTTTGGCAGTCTCTTTACCCGAGGATACAGTATA	758
Db	579	agagtggaaagctgtttcagggctctgaacctgaacctctttgggctggattgaccttggtt	638
Qy	759	TAGCTGGAGSCATTTCACACACTGAGAATGACCATCTTCTGCTCGTTCCTCCCTGCT	818
Db	639	ggtcatgatactgctacacagggattataaagattctgctaagaagacccaataagaa	698
Qy	819	CGTTATTGGCCATCTGTACACAGGAATCATAAAAACGGCTGCTGAGGTGCCCCAGTAAAAA	878
Db	699	gaataccaaagctgtccgtttgatttttggatcatcatcatcttttctctttggac	758
Qy	879	AAAGTACAGGCCACGCCGCTCATTTTTGTCAATGCGGTGTTTTTCATTTTCTGGAC	938
Db	759	ccctacaatttgactatacttattctgttttccaaagacttccgttccacccatgagt	818
Qy	939	ACCTACAATGTGGCTATCCTTCTCTCTTCCTATCAATCCATCTATTATGGAAATGACTG	998
Db	819	tgagcagacacacatttggacctggctgtgcaagtgacgaggtgatcgccactacgcga	878
Qy	999	TGAGCGGAGGAAGCATCTGGACCTGGTCATGCTGGTGACAGAGGTGATCGCCTACTCCCA	1058
Db	879	ctgctgtgccaacccagtgatctacgctctgttggtagagggttcgggaagtacctgcg	938
Qy	1059	CTGCTGCATGAACCCGGTGATCTAGCCCTTTTGTGGAGAGGTTTCGGAAAGTACCTGCG	1118
Db	939	gcagttgttccacagcgctgtggctgtgcacctggttaaatggctccccctctctccgt	998
Qy	1119	CCACTTCTTCCACAGGCATCTGCTCATGCACCTGGGAGATACATCCCATTCCTCTAG	1178
Db	999	ggacagcctggagagggtcagctccacatctccctccacaggggagcatgaactctctgc	1058
Qy	1179	TGAGAAGCTGGAAGAAGAACAGCTGTGCTCTCCATCCACAGCAGACCGCGAATCTCTAT	1238
Db	1059	tggggtt	1064
Qy	1239	TGTGTT	1244

RESULT 10

RESUL	IV
ID	T90384 standard: DNA: 2156 BP.

AC T90384;

DT 21-JAN-1998 (first entry)

DE Human MIP-1 alpha/RANTES receptor gene.

KW Macrophage inflammatory protein-1 alpha; MIP-1 alpha;

KW reduced upon activation normal T expressed and secreted; RANTES;

```

receptor; cytokine; antiinflammatory; inflammation; human; ss.
KW Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 63..1130
FT /*tag= a
FT
FT US5652133-A.
PN
PN 29-JUL-1997.
PD
PD 28-JAN-1993; 012988.
PF
PF 28-JAN-1993; US-012988.
PR
PR (US) US DEPT HEALTH & HUMAN SERVICES.
PA
PA Murphy PM;
PI WPI: 97-392945/36.
PI P-PSOB; W26588.
DR
DR MP-1-alpha and RANTES receptor nucleic acid - used to develop
PT products for the detection of these cytokine(s) and their receptors,
PT particularly in inflammatory processes
PT Claim 1; Column 11-16; 12pp; English.
PS
PS This nucleic acid sequence encodes a claimed receptor for macrophage
CC inflammation protein-1 alpha (MIP-1 alpha) and regulated upon
CC activation normal T expressed and secreted (RANTES) protein. Also
CC claimed are: (1) a subsequence of the nucleic acid, having at least
CC 12 contiguous nucleotides; (2) a cell transformed or transfected
CC with the nucleic acid; and (3) purified MIP-1 alpha/RANTES receptor
CC polypeptide. The products can be used for detecting the MIP-1
CC polypeptide. The products and polymorphisms in physiological samples.
CC In addition, the receptor can be expressed and used to assay for
CC MIP-1a/RANTES in biological samples. The quantitation of MIP-1
CC alpha/RANTES is useful for monitoring the levels of these cytokines
CC in a patient. Such measurements are useful in following the anti-
CC inflammatory effects of drugs and prospective usefulness of new anti-
CC inflammatory agents.
CC Sequence 2156 BP;
SQ 538 A; 547 C; 504 G; 567 T;
Query Match 25.1%; Score 424; DB 34; Length 2156;
Best Local Similarity 71.9%; Pred. No. 4.11e-281;
Matches 695; Conservative 0; Mismatches 271; Indels 0; Gaps

```

RESULT 10

RESUL	IV
ID	T90384
standard:	DNA: 2156 BP.

AC T90384;

DT 21-JAN-1998 (first entry)

DE Human MIP-1 alpha/RANTES receptor gene.

KW Macrophage inflammatory protein-1 alpha; MIP-1 alpha;

KW reduced upon activation normal T expressed and secreted; RANTES;

(ICOS-) ICOS CORP.
Gray PW, Raport CJ, Schweickart VL;
WPI: 97-341689/31.
P-PSDB: W27125.
New nucleic acid encoding chemokine receptors 88-2B and 88C - used
to modulate leukocyte trafficking, e.g. for treatment of
inflammation, tumours, viral infections, autoimmune diseases, etc.
Claim 47: Page 56-57: 65pp; English.
This sequence comprises a coding sequence for macaque chemokine
receptor 88C (W27125). It was isolated from macaque genomic DNA
using primers (see T85176-77) based on human 88C cDNA (see T85161).
The macaque 88C nucleotide sequence is 98% identical to that of
human 88C. 88C cDNAs can be used to produce recombinant
polypeptides in transformed host cells for use in the treatment of
e.g. atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
infection, AIDS and inflammatory conditions. Nucleic acid
fragments can be used to isolate genomic sequences, to detect
alleles of the gene (for diagnosis or in gene therapy), to alter
receptor genetics to facilitate identification of modulators and to
produce knockout animals, and (antisense forms) to alter/study the
genetics and expression of the receptor.
Sequence 1059 BP; 249 A; 274 C; 227 G; 309 T;
Query Match 13.3%; Score 225; DB 34; Length 1059;
Best Local Similarity 66.1%; Pred. No. 2.47e-136;
Matches 564; Conservative 0; Mismatches 279; Indels 10; Gaps 9;

PA 98 tgctcgcgtctactactcgtgttctctctgttgggttggtggaacacactggtctgcc 157
PI ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DR 290 TGCCCGCGCTTACTCCCTGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 349
DR ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 158 tcactcgtataaactgcaaaagcgtgaaagcatgactgacatcactcactcactcactg 217
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 350 TGATCTCTATAAATACAGGAGGCTCCGATTATGACACATCTACTGCTCAACCTGG 409
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 218 ccactctgactcgttct 276
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 410 CCAATTCGGACCTGCT 469
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 277 c-agtgggacttggaaatacaatgctgcaactctgacaggcctctatttataggct 334
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 470 ATAAGTGGGTTTGGCCATGGCATGCTGTAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 529
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 335 tctctctggaattcttctcactcctcctcctcctcctcctcctcctcctcctcctcct 394
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 530 TGTACAGGAGATCTTTTATAATCTGCTGCAATCGACAGTACTGCGCAATGCTC 589
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 395 atgctgtgttctttaaagccaggacagtcacacttgggtggtgacaaagtgtgatca 454
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 590 ATGCTGTGTGCTTTCGAGCCGCGACTGTCACATTTTGGTGTCATCACCAGCATCTGCA 649
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 455 ctgggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 514
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 650 CTTGGGCGCTGGCAGTGTAGCAGCTCTCTCTGAAATTTATCTTATGAGACTGA-AGAG 708
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 515 aaggtcttcattacact-gcagctctcatttccatcacagt-cagtatcaattctgaa 572
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 709 TTGTTTGAAGAGACTCTTTGAGTGCTCTTTTACCCAGGATACAGATATATAG-CTGGAG 767
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 573 gaatttcagacataaagatggttcattctggggtggtggtggtggtggtggtggtggtggt 632
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 768 GCATTTCCACACTCTGAGATGACCATCTCTCTGTCGTCTCTCTCTCTCTCTCTCTCTCT 827
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 633 catctgactcgggaatctctgaaaaactcgtctcgtggtggtggtggtggtggtggtggtggt 692
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 828 CATCTGTACACAGATCATCAAAAGCGCTGCTGAGGTGCGCCAGTAAAAA-AA-AGT-A 884
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 693 caggcgtgaggtctattcaccatcatgattgttttttttttttttttttttttttttttttt 752
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 885 CAAGGCCATCCGGCTCATTTTGTTCATCATGGCGGTGTTTTCATTTCTTGGACACCTTA 944
QY ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 753 caacattgtctctctcctgaacacctccaggaaattcttggcctgtaataattgtagtag 812
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 945 CAATGTGGCTATCCT 1004
DB 813 cttaacagggttgagacaagcagcagtgagtgagagagactcttgggatgacacactgctg 872
QY 1005 GAGCAAGACATCTCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1064
DB 873 catcaaccccccatcatgct 932
QY 1065 CATGACCCCGGTGATCTACGCCCTTGTGGAGAGAGGTTCCGGAAGTACCTGCGCCACTT 1124
DB 933 ctctccaaagcac 945
QY 1125 CTTCCACAGGCAC 1137

RESULT 13
ID T76920 standard; cDNA; 1225 BP.
AC T76920;
DT 08-JUN-1998 (first entry)
DE DNA encoding human CC chemokine receptor 5 (CCR5).
KW CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW human immunodeficiency virus; HIV; CD4; AIDS; therapy;
KW transgenic animal; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 27..1085 /*tag= a
FT W09745543-A2.
PD 04-DEC-1997.
PF 28-MAY-1997; U09586.
PR 28-MAY-1996; US-018508.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Alkhatib G, Berger EA, Broder CC, Combadiere C,
PI Feng Y, Kennedy PE, Murphy PM;
DR WPI: 98-032650/03.
DR P-PSDB: W23835.
PT CC chemokine receptor 5 polypeptide - used to inhibit membrane
PT fusion between HIV and a target cell
PT Claim 15; Fig 1C; 70pp; English.
CC This DNA sequence codes for a novel human macrophage-selective CC
CC chemokine receptor (see W23835) designated CCR5. It was isolated
CC from a lambda gt11 cDNA library. Another isolated DNA molecule (see
CC T76919) codes for an Alal27Leu variant (see W23834) of CCR5. The
CC susceptibility of human macrophages to HIV infection depends on
CC cell surface expression of the human CD4 molecule and CCR5. CCR5
CC is a member of the 7-transmembrane superfamily of G-protein
CC coupled cell surface molecules. It plays an essential role in the
CC membrane fusion step of infection by some HIV isolates. The
CC establishment of stable, non-human cell lines and transgenic
CC mammals having cells that coexpress human CD4 and CCR5 provides
CC valuable tools for research of HIV infection. Antibodies that bind
CC to CCR5, CCR5 variants, and CCR5-binding agents capable of blocking
CC membrane fusion between HIV and target cells represent potential
CC anti-HIV therapeutics for macrophage tropic strains of HIV.
CC Antisense oligonucleotides can also be used to inhibit expression
CC of CCR5 in a cell.
SQ Sequence 1225 BP; 289 A; 302 C; 280 G; 354 T;
Query Match 13.2%; Score 222; DB 39; Length 1225;
Best Local Similarity 65.4%; Pred. No. 3.54e-134;
Matches 557; Conservative 0; Mismatches 287; Indels 8; Gaps 7;

DB 124 tgctcgcgtctactcactcgtgttctctctctctctctctctctctctctctctctctct 183
QY 290 TGCCCGCGCTGTAATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 349
DB 184 tcactcgtataaactgcaaaagcgtgaaagcagcagcagcagcagcagcagcagcagcag 243
QY 350 TGATCTCTATAAATACAGGAGGCTCCGAAATATGACCAACATCTACCTGCTCAACCTGG 409
DB 244 ccactctgactcgtttttct 302
QY 410 CCAATTCGGACCTGCT 459

Db	303	c--agtgggactttggaatacaaatggtcgaactcttgacagggtctctattttataggct	360
Qy	470	ATAACTGGGTGTTTGCCATGGCATGTGTAAGCTCCTCTCAGGGTTTTATCACACAGGCT	529
Db	361	tcctctcgaatactcttcacatcctctcgaatacgataggtacotggctctctctcc	420
Qy	530	TGTACAGGAGATCTTTTTTCATAACTCTGCTGACAAATCGACAGGTACTGTGCCAATTGTCC	589
Db	421	atgctgtgtttgctttaaaagccaggacggtcacctcttgggggtgagaaagtgtgatca	480
Qy	590	ATGCTGTGTTGGCCCTCGAGCCGGACATGTCACATTTGGTGTCAATCACAGCATCGTCA	649
Db	481	cttgggtggtgggtgtgttgggtctctccccagggaatcaatctttaccagatctcctcaaaag	540
Qy	650	CCTGGGCCCTGGCAGTGTCTAGCAGCTCTCTCCGTGAATTTATCTCTATGAGACTGAAGAGT	709
	541	aaggctcttcattacacctgcagctctcatttccatacagt-cagtatcaattctggaag	599
Qy	710	TGTTTGAAGAGACTCTTTGCGAGTGTCTTTTACCAGGAGATACAGTATATAG-CTGGAGG	768
Db	600	aattccagacattaaagatagtcattcttggggctggctgcgcgtcgtctgtcatgctgc	659
Qy	769	CATTTCACACTCTGAGATGACCATCTCTGTCGTCTCTCCCTCTGCTCGTTATGSCC	828
Db	560	atctgctactcgggaatcctctaaaaactctgctctcgggttcgaaatcgagaagaagagcac	719
Qy	829	ATCTGTCTACAGAGGAATCATCAAAACGGCTGCTGAGGTGCCCCAGTAAAAA-AA-AGT-AC	885
Db	720	agggcttgaggcttatcttcaccatcatgattttatttctctctctcgtggctccctac	779
Qy	886	ANGGCCATCCGGTCAATTTTGTFCATCATGGCGGTGTTTTTCATTTCTCGACACCCCTAC	945
Db	780	aacattgctctctctcgaacacctccaggaaattctttggcctgaaataaattgcagtagc	839
Qy	946	AATGTGGCTATCTCTCTCTTCTCCATCAATCCATCTTATTTGGAAATGACTGTGAGCGG	1005
Db	840	tctaaaggttggaaccaagctatgcaggtgcagagagactcttggagatgaacgaactgtctgc	899
Qy	1006	ACGAAGCATCTGAGACCTTGCTCATGTGGTGGACAGAGGTGATGCCCTACTCCCACTGTCTGC	1065
Db	900	ataacccccatcatgctcttctcgagggagaagttcagaataacctctcttagtcttc	959
Qy	1066	ATGAACCCGGTGATCTACGCCCTTTGTTGGAGAGAGGTTCCGGGAAGTACTCTGGCCACTTC	1125
	960	ttccaaaagcac	971
Qy	1126	TTCCACAGGCAC	1137

```

RESULT 14
ID    T76919 standard; cDNA; 1255 BP.
AC    T76919;
DT    08-JUN-1998 (first entry)
DE    DNA encoding human CC chemokine receptor 5 (CCR5) A127L variant.
KW    CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW    human immunodeficiency virus; HIV; CB4; AIDS; therapy;
KW    transgenic animal; ss.
OS    Homo sapiens..
FH    key          Location/Qualifiers
FT    CDS          1..1116
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                WO9745543-A2..
                04-DEC-1997.
                PD
                PF    28-MAY-1997; U09586.
                PR    28-MAY-1996; US-018508.
                PA    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                PI    Alkhatib G, Berger EA, Broder CC, Combadiere C,
                PI    Feng Y, Kennedy PE, Murphy PM;
                PI    WPI: 98-032650/03.
                DR    P-PSDB: W23834.
                CC chemokine receptor 5 polypeptide - used to inhibit membrane
                fusion between HIV and a target cell

```

PS Claim 15; Fig 1B; 70pp; English.

CC This DNA sequence codes for an Alal27leu variant (see W23834)

CC of a novel human macrophage-selective CC chemokine receptor (see

CC also W23835) that has been designated CCR5. It was isolated from a

CC lambda gtl1 cDNA library. The conservative amino acid substitution

CC should not affect the biological activity of CCR5. The

CC susceptibility of human macrophages to HIV infection depends on

CC cell surface expression of the human CD4 molecule and CCR5. CCR5

CC is a member of the 7-transmembrane superfamily of G-protein

CC coupled cell surface molecules. It plays an essential role in the

CC membrane fusion step of infection by some HIV isolates. The

CC establishment of stable, non-human cell lines and transgenic

CC mammals having cells that coexpress human CD4 and CCR5 provides

CC valuable tools for research of HIV infection. Antibodies that bind

CC to CCR5, CCR5 variants, and CCR5-binding agents capable of blocking

CC membrane fusion between HIV and target cells represent potential

CC anti-HIV therapeutics for macrophage tropic strains of HIV.

CC Antisense oligonucleotides can also be used to inhibit expression

CC of CCR5 in a cell.

CC Sequence 1255 BP: 295 A; 311 C; 289 G; 360 T;

SQ

Query Match	13.28;	Score 222;	DB 39;	Length 1255;
Best Local Similarity	65.44;	Pred. No. 3.54e-134;		
Matches	557;	Conservative 0;	Mismatches 287;	Indels 8; Gaps 7;
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Qy	290	TGCCCCGCGTGTACTCCCTGGTGTCTACTCTGGCCCTCTTGGGCATGTGGTGGTGA	349	
Db	215	tcattcctgataaaactgcacaaaggctgaagcagcagctgacatctaccctgcctcaacctgg	274	
Qy	350	TGATCCTCATAAAATACAGGAGGCTCGAATTATGACCAACATCTACCTGCTCAACCTGG	409	
Db	275	ccattctgacctgttttttcttactgtccctctctgggtcctcaactactt--ggccgc	332	
Qy	410	CCATTTCCGACCTGCTCTCTCTCGTCACCTTCATTTGGATGCCATGTGTCAAGGGGC	469	
Db	333	ccag-tgggactctggaatcacaaatgctcaactcttcagcagggctctatttataggct	391	
Qy	470	ATAACTGGGTTTTGGCCATGGCATGTGTAAAGTCTCTCTCAGGGTTTTATCACACAGGCT	539	
Db	392	tcttctctggaactcttcttcatcctctctgcacatcgataggtacctgctggtggtcc	451	
Qy	530	TGTACAGCGAGATCTTTTTCATATCTGCTGCAATCGACAGGTACTTGCCTATTGTCC	589	
Db	452	atgctgtgtttgttttaaaagcagcagcggctcacccttgggggtgggagcaagtgtatca	511	
Qy	590	ATGCTGTGTTTGCCCTTCGAGCCGGACTGCTACTTTTGGTGTATCATCACAGCATGCTCA	649	
Db	512	cttgggtggtcgtgtgtttgctgctctccaggaatcatctttaccagatctcctcaaaaag	571	
Qy	650	CTCGGGCCTGGCAGTGCCTAGCAGCTCTTCTGAAITTAITCTCTATGACACTGAAAGT	709	
Db	572	aaggctcttcattacacctgcagctcattttccatacagt-cagtatcaattctggaag	630	
Qy	710	TGTTTGAAGAGACTCTTTTGCAGTGTCTTTTACCAGAGGATACAGTATATAG-CTGGAGG	768	
Db	631	aatttcagacattaaagatagtcattcttgggctggtcgcgtgcgtgtgtcatggtc	690	
Qy	769	CATTTCACACTCTGAAATGACCATCTCTGTCTCGTCTCTCCTCTGCTGCTGTTATGGCC	828	
Db	691	atctgctactcgggaactctaaaaactcgtctcgtggtcgaatgagaagaagagcac	750	
Qy	829	ATCTGCTACAGGAATCATCAAAACGCTGCTGAGGTGCCCCAGTAAAAA-AA-AGT-AC	885	
Db	751	agggctgtgaggcttatcttcacatcatgattgttttattttctctcttgggctccctac	810	
Qy	886	AAGGCCATCGGCTCAITTTTGTTCATCATGCGGTGTTTTTCATTTTCTGGACACCTAC	945	
Db	811	aaeatgtctctctctcgaacacctccaggaattcttggcctggaataattgcagtagc	870	
Qy	946	AATGTGCTATCTCTCTCTCTCTATCAATCCATCTCTATTGGAAATGACTGTGACGG	1005	

[illegible]

(TM)

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ch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Wed Dec 9 00:18:36 1998; MasPar time 1546.71 Seconds
Tabular output not generated. 1381.249 Million cell updates/sec

Title: >US-08-963-656-3

Description: (1-1193) from US08963656.seq

Perfect Score: 1193

N.A. Sequence: 1 TTGCTGTTATCCGGCAAGA.....TTGCCCTAAGAGGAGGACC 1193

Comp: AACACGAATAGCCCCCTTCT.....AACGGATTCTCCTCTCTGG

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl-est55

Database: genbank-est107

1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3
5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13
10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17
14:gb_est18 15:gb_est19 16:gb_est20 17:gb_est21
18:gb_est22 19:gb_est23 20:gb_est24 21:gb_est25 22:gb_est26
23:gb_est27 24:gb_est28 25:gb_est29 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4

Statistics: Mean 11.267; Variance 1.874; scale 6.013

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description	Pred. No.
1	204	17.1	450 20	W04836	
2	119	10.0	542 8	AA57303	
3	117	9.8	447 11	AA671573	
4	69	5.8	252 12	AA754459	
5	56	4.7	252 12	AA754459	
6	50	4.2	247 12	AA754458	
7	50	4.2	469 27	B84215	
8	48	4.0	247 12	AA754458	
9	39	3.3	2275 11	AF034173	
10	36	3.0	456 25	AA354393	
11	35	2.9	553 26	FR0019847	
12	34	2.8	529 23	AA177828	
13	33	2.8	539 25	FR0019844	

33	2.8	602 7	AA511931	vgl7f07.r1 Soares mous	8.28e-21
32	2.7	310 19	N70844	za73h08.s1 Homo sapien	4.40e-19
32	2.7	507 12	AA795654	Homo sapiens ntcon2 co	4.40e-19
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31	2.6	391 23	AA153412	mp93c11.r1 Soares 2NDM	2.20e-17
31	2.6	484 23	AA120018	vr14h02.r1 Barstead mo	2.20e-17
31	2.6	639 12	AA816049	mt83f01.r1 Soares mous	2.20e-17
31	2.6	793 22	AA182270	ym31f07.r1 Homo sapien	1.03e-15
30	2.5	249 16	H29103	EST62304 Jurkat T-cell	1.03e-15
30	2.5	380 25	AA354040	EST222608 Normalized r	1.03e-15
24	2.5	604 18	AI178926	Y143e08.s1 Homo sapien	4.45e-14
26	2.4	128 16	H24894	ATH362 HTCDL1 Homo sap	4.45e-14
29	2.4	242 13	T25959	ne38f06.s1 NCI_CGAP_Ki	4.45e-14
29	2.4	249 8	AA494496	EST52629 Fetal heart I	4.45e-14
28	2.4	252 25	AA346471	EST52623 Homo sapiens	4.45e-14
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32	2.4	354 15	AA954002	zo80f07.r1 Stratagene	4.45e-14
33	2.4	429 22	AA159773	CIT-HSP-2344P12.1F CIT	4.45e-14
34	2.4	437 27	AQ055410	zo80f07.s1 Soares para	4.45e-14
35	2.4	450 21	W37302	qb89p03.x1 Soares_feta	4.45e-14
36	2.4	460 22	AA159668	ac83f12.s1 Stratagene	4.45e-14
37	2.4	465 17	AI097155	Oz40a07.s1 NCI_CGAP_Ki	4.45e-14
38	2.4	475 11	AA679851	Oj19e07.s1 NCI_CGAP_Ki	4.45e-14
39	2.4	478 15	AA978343	nc42g06.s1 NCI_CGAP_Pr	4.45e-14
40	2.4	481 18	AA878538	ns64a08.s1 NCI_CGAP_Pr	4.45e-14
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ALIGNMENTS

RESULT 1	W04836	450 bp	mRNA	EST	23-APR-1996
LOCUS	zab1f05.r1 Soares fetal lung NBH19W Homo sapiens cDNA clone 298977				
DEFINITION	5' similar to gb:D10925 C-C CHEMOKINE RECEPTOR TYPE 1 (HUMAN); mRNA sequence.				
ACCESSION	W04836				
NID	12777557				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 450)				
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.				
TITLE	The WashU-Merck EST Project				
JOURNAL	Unpublished (1995)				
COMMENT	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 850L, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Seq primer: mob.REGA-ET High quality sequence stop: 402. Location/Qualifiers 1. .450 /organism="Homo sapiens" /note="organ: lung; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st				

FEATURES

source


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RESULT 3
LOCUS AA671573 447 bp mRNA EST 25-NOV-1997
DEFINITION v104g01.r2 Soares mouse mammary gland NDMMG Mus musculus cDNA clone
963216 5' similar to TR:G1322040 G1322040 C-C CHEMOKINE RECEPTOR.
; mRNA sequence.
ACCESSION AA671573
NID 92643652
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
AUTHORS Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 447)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:552008
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 397.
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Location/Qualifiers
1..447
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Organ: mammary gland; Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site.1: Not I;
Site.2: Eco RI; 1st strand cDNA was primed with a Not I -
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TGTTACCAATCTGAGTGGGAGCGGCCCGAATGCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
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/db_xref="taxon:10090"
/clone="963216"
/clone_lib="Soares mouse mammary gland NDMMG"
/sex="male"
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BASE COUNT 104 a 102 c 92 g 149 t
ORIGIN
Query Match 9.8%; Score 117; DB 11; Length 447;
Best Local Similarity 66.0%; Pred. NO. 1.32e-203;
Matches 293; Conservative 0; Mismatches 146; Indels 5; Gaps 5;
Db 5 TCACAGGCGCTATACATGTTGTTATTTGGTGGAACTCTTTCATATCTCTCCCTGACAA 64
QY 417 TCTCAGGGTTTATACACAGCGCTGTACAGGAGATCTTTTTCATATCTCTGTCGACAA 476
Db 65 TTGATAGGTACTTGCTATGTCATGCTGTGTTTGTCTTTAAAGTCAGAACGGTCAACT 124
QY 477 TCGACAGGTACCTGGCCATGTCATGCTGTGTTTCCCTTCGAGCCGCGACTGTCACTT 536
Db 125 TTGGGGTGATACACAGTGTAGTCATCTGGCGGTGGCTGTGTTGCTCTCTCCCGAGAA 184

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QY 537 TTGGTGTCTATCACCAGCATCTCACCCTGGCGCTGGCAGTCTCTTCTCGAAT 596
Db 185 TAATCTTTTACCAGATCTTCAGAAAGAGGTTTTCATATATACATGTCAGTCTCTCATTTTCAC 244
QY 597 TTATCTTCTATGAGATGAAGAGTGTGTTGAAGAGACATCTTTGTCAGTGTCTCTTTTACCAG 656
Db 245 ACACAT-CAGTATCATCTTCTGGAAGAGTTTCCAAACATTTAAAGATGGTTCATCTTGAGCCGTG 303
QY 657 AGGATACAGTAT-ATAGCTGGAGGCAATTTCCACACTCTGAGAATGACCATCTTCTGTCTC 715
Db 304 ATCTCTGCTCTACTGTCTCATGTCATCTGCTACTCTAGGAAATTTCTCCACACCTCTGTTTGGC 363
QY 716 GTTCTCCCTCTGCTGTTATGGCCATCTGCTACAGAGATCATCAAAACGCTGCTGAGG 775
Db 364 TGTAGGAATGAGAAGAGGACAGGCTGTGAGGCTCATCTTTTGCCATCATGATTGTC 423
QY 776 TGCCCCCAGTAAAAA-AA-AGT-ACAAGGCCATCCGGCTCATTTTGTCTCATCATGCGCGTG 832
Db 424 TACTTTCTCTTCTGGACATCCCTAC 447
QY 833 TTTTTCATTTTCTGGACACCCCTAC 856
RESULT 4
LOCUS AA754459 252 bp mRNA EST 20-JAN-1998
DEFINITION 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
cDNA clone 97SN1787, mRNA sequence.
ACCESSION AA754459
NID 92801165
KEYWORDS EST.
SOURCE Rice.
ORGANISM Oryza sativa
REFERENCE Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
AUTHORS Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
1 (bases 1 to 252)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,B.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
TITLE
JOURNAL
COMMENT
Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeunesun20.astl.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahebio@server.myongji.ac.kr
Seq primer: M13 Reverse Primer.
FEATURES
Location/Qualifiers
1..252
/organism="Oryza sativa"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="97SN1787"
/tissue.type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
BASE COUNT 5 a 21 c 12 g 35 t 179 others
ORIGIN
Query Match 5.8%; Score 69; DB 12; Length 252;
Best Local Similarity 13.8%; Pred. No. 1.55e-93;
Matches 33; Conservative 125; Mismatches 76; Indels 5; Gaps 5;

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Db 15 CBAMTTSYBCHGNBVCVASHGNYMSVHNCBTRGTHCDCKKNVNSMTWGTWNBVNS 74
Qy 327 CGGACCTCTCTTCTGCTGACCTTCCATCTGATCCATATGTCAGGGGGATAACT 386
Db 75 GDHWYBVBNTKVDYGNHTRCNRWBVTRMAHYHDYTNBNNNDYHMHBBMYBBTGC 134
Qy 387 GGGTTTTTGGCCATGGCATGTGTAAGCTCCTCAGGGTTTATACACACA-GGCTTGATC 445
Db 135 MTCNMCWBHYNKTC-TASGWHSTSNYDVKS-STNTWGTBTSYDKSMHGYWCSBBVKYHT 192
Qy 446 AGCGAGATCTTTTTCATATCTGCTGACATCGACAGTACCTGGCCATGTGTCATGCT 505
Db 193 KVSITRATRSYTCVRKYCVW-WMTKKVY-KKYHVVBBCSHCHTDSKCKTMMWTKNKHVMTS 249
Qy 506 GTGTTTGCCCTTCGAGCCCGGACTGTCACTTTTGTGTGTCATCACCAGCATCGTCACCTG 564

RESULT 5
LOCUS AA754459 252 bp mRNA EST 20-JAN-1998
DEFINITION 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
ACCESSION AA754459
NID 92801165
KEYWORDS EST.
SOURCE rice.
ORGANISM Oryza sativa
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
REFERENCE 1 (bases 1 to 252)
AUTHORS Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
JOURNAL
COMMENT
Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
FEATURES
source
1..252
/organism="Oryza sativa"
/cultivar="Milyang23"
/notes="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="97SN1787"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
BASE COUNT 5 a 21 c 12 g 35 t 179 others
ORIGIN
Query Match 4.7%; Score 56; DB 12; Length 252;
Best Local Similarity 8.3%; Pred. No. 1.28e-65;
Matches 19; Conservative 122; Mismatches 84; Indels 3; Gaps 3;
Db 23 YBCHGNBVCVASHGNYMSVHNCBTRGTHCDCKKNVNSMTWGTWNBVNSGDHVBV 82
Cp 251 CCACATGCCCAAGAGCCCACTGACACACAGGAGTACAGCGGGGGACCAACTGGG 192
Db 83 BNTKVDYGNHTRCNRWBVTRMAHYHDYTNBNNNDYHMHBBMYBBTGCMTCT-MWC 141
Cp 191 CCATCAGTCTCTGATACCTTTTTCACAGACAGCCCATCATGATGATGATG 132

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Db 142 WBHNTKCTASGHTSTNVDKS-STNTWGTBTSYDKSMHGYWCSBBVKYHKVSTTRAT 200
Cp 131 TGGTACCAAGGTCCTCACTGATCTAGTGGTGGTTCATTCCTCCCTGAAAAATC 72
Db 201 RSYTCVKYCVMMTKVKVKKYHVVBGCHBTDSKCKTMMWTKNKHVMT 248
Cp 71 TCITCTAAGTAAAC-CGGACGGTGGTCTTCTATTGTATTTCGAT 25

RESULT 6
LOCUS AA754458 247 bp mRNA EST 20-JAN-1998
DEFINITION 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
ACCESSION AA754458
NID 92801164
KEYWORDS EST.
SOURCE rice.
ORGANISM Oryza sativa
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
REFERENCE 1 (bases 1 to 247)
AUTHORS Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
JOURNAL
COMMENT
Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
FEATURES
source
1..247
/organism="Oryza sativa"
/cultivar="Milyang23"
/notes="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="97SN1784"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
BASE COUNT 7 a 16 c 21 g 34 t 169 others
ORIGIN
Query Match 4.2%; Score 50; DB 12; Length 247;
Best Local Similarity 12.3%; Pred. No. 3.17e-53;
Matches 28; Conservative 104; Mismatches 94; Indels 1; Gaps 1;
Db 1 HWDCTMNTVVRGCCCBANWKNKHTHMTBWCVRVRVTGTTNNGKNGRTTWNDCSDNA 60
Qy 876 CTTCTCATCAATCCATCTTATTGGAATGACTGTGAGCGGAGCAAGCATCTGGACCTGG 935
Db 61 HCRVTBWWYARSKYGYGTBYISWNVDTNTGGTGVGTGTTNVHSGWNNRCSNSVYVWBT 120
Qy 936 TCATGCTGGTGACAGAGGTGATCGCTACTCCACACTGCTGCATGACCCCGGTGATCTAGC 995
Db 121 AYCDYBHYBDR-ANHVDFTCTNDRGVYCNVTASDNGTSATKRVYTGVDKTDSCGGGCMRW 179
Qy 996 CCTTTGTTGGAGAGAGGTTCCGGAAGTACCTGCGCCACTCTCTCCACAGCACTTGCTCA 1055
Db 180 VTGSSBYBCGVNVVYRTTSMKTDKSTKMBSDMSRSHVHYGRWM 226

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REFERENCE 2 (bases 1 to 2275)
 AUTHORS Tripodis,N. and Ragoussis,J.
 TITLE Direct Submission
 JOURNAL Submitted (13-NOV-1997) Division of Medical and Molecular Genetics,
 Guy's Hospital, 7th floor, Guy's Tower, London SE1 9RT, UK

FEATURES
 Location/Qualifiers
 1..2275

source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p21.3"
 /clone="ntcon2 contig"
 /tissue="liver; brain"
 /dev_stage="fetus"
 /note="similar to Br140"

BASE COUNT 438 a 619 c 470 g 599 t 149 others

ORIGIN

Query Match 3.3%; Score 39; DB 11; Length 2275;
 Best Local Similarity 9.6%; Pred. No. 1.15e-31;
 Matches 16; Conservative 87; Mismatches 64; Indels 0; Gaps 0;

1482 RWKRRKRRKRRMTGWYKRYMAMMACMACWYWKYKMKKWKYKRYKRYKTY 1541

QY 462 TAATCCTGTCGACATCGACAGGTACCTGGCCATGTCCATGCTGTGGCCCTTCAG 521

Db 1542 YKSWRYWYTYTYWYCWCTSMKASACAMRWYMGSRSSRYWYWSMCGYGMT 1601

QY 522 CCGGACGTGTCATTTTGTGTGTCATCAGCATGCTCACCTGGGCGCTGGCAGTGC 581

Db 1602 KRYRYSWTGWTKTWYKMSMTWTWYTYTWWTWTTTWTWTTTWWWW 1648

QY 582 CAGCTTCTCGAATTTATCTTCTATGAGACTGAAGAGTGTGTTGAA 628

RESULT 10
 LOCUS AA354393 456 bp mRNA EST 21-APR-1997
 DEFINITION EST62864 Jurkat T-cells V Homo sapiens cDNA 5' end similar to
 guanine nucleotide-binding protein HM89, mRNA sequence.

ACCESSION AA354393

NID 92006897

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominidae;
 Homo.

REFERENCE 1 (bases 1 to 456)
 AUTHORS Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,
 Bult C.J., Lee N.H., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
 White O., Sutton G., Blake J.A., Brandon R.C., Man-Wai C.,
 Clayton R.A., Cline T.R., Cotton M.D., Earle-Hughes J., Fine L.D.,
 Fitzgerald L.M., Fitzhugh W.M., Fritchman J.L., Geoghagen N.S.,
 Glodok A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle P.S., Jr.,
 Kelley J.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M.,
 Moreno-Palauques R.F., McDonald L.A., Nguyen D.T., Pelligrino S.M.,
 Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley R.,
 Small K.V., Spriggs T.A., Utterback T.R., Weidman J.F., Li Y.,
 Bednarek D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.J.,
 Dimke D., Feng D.-F., Ferlie A., Fischer C., Hastings G.A.,
 He W.W., Hu J.S., Greene J.M., Gruber J., Hudson P., Kim A.K.,
 Kozak D.L., Kunsch C., Hungjun J., Li H., Weissner P.S., Olsen H.,
 Raymond L., Wei Y.F., Wang J., Xu C., Yu G.L., Ruben S.M.,
 Dillion P.J., Fannon M.R., Rosen C.A., Haseltine W.A., Fields C.,
 Fraser C.M. and Venter J.C.

TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE 96026280

COMMENT Other_ESTs: THC166975

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 301869056

Fax: 3018699423

Email: arkerlavet@tigr.org

For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/cdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1..456

/organism="Homo sapiens"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

XhoI"

/db_xref="ATCC (inhost):154827"

/db_xref="taxon:9606"

/clone_lib="Jurkat T-cells V"

/cell_type="T-lymphocyte"

<1..456

BASE COUNT 116 a 121 c 105 g 111 t 3 others

ORIGIN

Query Match 3.0%; Score 36; DB 25; Length 456;

Best Local Similarity 61.1%; Pred. No. 3.88e-26;

Matches 96; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Db 186 TGCCACACATCTACTCCATCATCTTTACTGCGATTGTGGCAATGGATGTGTCATCC 245

QY 201 TGCCCCGGCTGCTCCCTGTTGTTCTACTGTGGGCTCTTGGGCAATGTGGTGGTGA 260

Db 246 TGGTCATGGGTTACCAGAGAACTGAGACCATGACGGCAAGTACAGGTGCACCTGT 305

QY 261 TGATCCCATAAATACAGGAGTCCGAAATATGACCAACATCTACTGTCAACCTGG 320

Db 306 CAGTGGCGACCTCTCTTTNTCATCAGCTTCCCTT 342

QY 321 CCAATTCGGACCTCTCTTCTCTGTCACCTTCCATT 357

RESULT 11

LOCUS FR0019847 553 bp DNA GSS

DEFINITION F.rubripes GSS sequence, clone 036L10a44, genomic survey sequence.

ACCESSION AL012734

NID 92679102

KEYWORDS GSS; genome survey sequence.

SOURCE Fugu rubripes.

ORGANISM Fugu rubripes

Eukaryotes; Metazoa; Chordata; Vertebrata; Actinopterygii;

Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;

Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.

REFERENCE 1 (bases 1 to 553)

AUTHORS Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrana, Y.,

Williams, G. and Brenner, S.

TITLE Direct Submission

JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource

Centre HinXon, Cambridge, CB10 1SB. Email: biohelp@hgm.mrc.ac.uk

COMMENT Vector: pBluescript II KS

V_type: phagemid

PRIMER: KS

DESCR: One pass dye-terminator sequencing of cosmid cloned genomic

sequence.

Location/Qualifiers

1..553

/organism="Fugu rubripes"

/db_xref="taxon:31033"

/clone_lib="cosmid 036L10"

/clone="036L10a44"

BASE COUNT 108 a 157 c 126 g 144 t 18 others

ORIGIN

Query Match

Best Local Similarity 2.9%; Score 35; DB 26; Length 553;

Matches 58; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Db 331 GAAGCTGCACAGCAGCATCTACCTGACTCACCTGGCGCTGGCGGACCTCCTCTT 390
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Qy 280 GAGGCTCCGAATATGACCAACATCTACCTGCTACCTGGCCATTTCCGACCTGCTCTT 339
|||||
Db 391 CGGCTTACCCCTGCTTCTGG 412
|||||
Qy 340 CCGTGCACCCCTCCATTCGG 361
|||||

RESULT 12
LOCUS AA177828 529 bp mRNA EST 16-FEB-1997
DEFINITION mt07f02.r1 Soares mouse 3DMS Mus musculus cDNA clone 620379 5'
similar to TR:G663021 G663021 PROTEINASE ACTIVATED RECEPTOR 2.; ;
mRNA sequence.
ACCESSION AA177828
KEYWORDS 91759090
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 529)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The washU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:381203
Seq primer: -28Mj3 rev2 from Amersham
High quality sequence stop: 494.
FEATURES
Location/Qualifiers
1..529
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGCGCTGTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M.Fatima Bonaldo."
/db_xref="taxon:10090"
/clone="620379"
/clone_lib="Soares mouse 3DMS"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
<1..>529
BASE COUNT 110 a 168 c 107 g 144 t
ORIGIN

Query Match 2.8%; Score 34; DB 23; Length 529;
Best Local Similarity 63.2%; Pred. No. 1.46e-22;
Matches 117; Conservative 0; Mismatches 65; Indels 3; Gaps 2;

mRNA
BASE COUNT 110 a 168 c 107 g 144 t
ORIGIN

Db 134 CAACCTGCCATGCAGATCTCCTTTCTGTGTCACTGCCATTAAAGTCGCCTACCA 193
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Qy 313 CAACCTGCCATTTCCGACCTGCTCTTCTGTCACCTTCATCTCTGATC--C-ACTA 369
|||||
Db 194 TCTCAATGCCAACAACTGGGTATTTGGCGAGGTACAGTCCGCGGATCACACGGTTGTTTT 253
|||||
Qy 370 TGTACGGGGGCATAACTGGTTTTTTGGCCATGGCATGTGAAGCTCCTCTCAGGGTTT 429
|||||
Db 254 CTACGGCAACATGTAATCTGCTATCTCTACCTGTCATGGGCATCAACCGCTACT 313
|||||
Qy 430 TCACACAGGCTGTGACAGGAGATCTTTTTCATATCTGCTGACAATCGACAGTACT 489
|||||
Db 314 GGCCA 318
|||||
Qy 490 GGCCA 494
|||||

RESULT 13
LOCUS FR0019844 539 bp DNA GSS 10-DEC-1997
DEFINITION F.rubripes GSS sequence, clone 036L10aB4, genomic survey sequence.
ACCESSION AL012731
KEYWORDS 92679099
SOURCE GSS; genome survey sequence.
ORGANISM Fugu rubripes.
REFERENCE 1 (bases 1 to 539)
AUTHORS Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrana,Y.,
Williams,G. and Brenner,S.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
COMMENT Vector: pBluescript II KS
Vtype: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
FEATURES
Location/Qualifiers
1..539
/organism="Fugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 036L10"
/clone="036L10aB4"
BASE COUNT 123 a 155 c 128 g 111 t 22 others
ORIGIN

Query Match 2.8%; Score 33; DB 26; Length 539;
Best Local Similarity 67.1%; Pred. No. 8.28e-21;
Matches 57; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Db 141 GCANGCGGTCCGGAACTCACCCCGATGAGGCGCTACACCGGATTCACNGCGCAGT 200
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Cp 1028 CGAGTACTTCGGAACTCTCTCCAAAGGCGGTAGATCACCGGTTCTGCACGACT 969
|||||
Db 201 GCACAAAGGCCANCACTTGGTGAC 225
|||||
Cp 968 GGGAGTAGCGGATCACCCTCTGTAC 944
|||||

RESULT 14
LOCUS AA511931 602 bp mRNA EST 08-JUL-1997
DEFINITION vg17f07.r1 Soares mouse NBMH Mus musculus cDNA clone 861637 5'
similar to gb:L19315 CHOLECYSTOKININ TYPE A RECEPTOR (HUMAN);, mRNA
sequence.
ACCESSION AA511931
KEYWORDS 92249785
SOURCE EST.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 602)
AUTHORS Soares,B., Wilson,R. and
Waterston,R.
TITLE The washU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:381203
Seq primer: -28Mj3 rev2 from Amersham
High quality sequence stop: 494.
FEATURES
Location/Qualifiers
1..529
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGCGCTGTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M.Fatima Bonaldo."
/db_xref="taxon:10090"
/clone="620379"
/clone_lib="Soares mouse 3DMS"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
<1..>529
BASE COUNT 110 a 168 c 107 g 144 t
ORIGIN

Query Match 2.8%; Score 34; DB 23; Length 529;
Best Local Similarity 63.2%; Pred. No. 1.46e-22;
Matches 117; Conservative 0; Mismatches 65; Indels 3; Gaps 2;
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Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Mus.
1 (bases 1 to 602)
Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
Theising B., Wyllie T., Lennon G., Soares B., Wilson R. and
Waterston R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:505725
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 388.
Location/Qualifiers
1. .602
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGGAAAGTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Minoru KO, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
/db_xref="taxon:10090"
/clone="861637"
/clone_lib="Soares mouse NBMH"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
1. .>602
142 a 164 c 144 g 152 t
mRNA
BASE COUNT 142 a 164 c 144 g 152 t
ORIGIN
Query Match 2.8%; Score 33; DB 7; Length 602;
Best Local Similarity 64.6%; Pred. No. 8.28e-21;
Matches 73; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
Db 324 CTGTACTCTTCATATTCCTCTCAGTGTCTGGGGAACACGCTGGTATACAGGTCTG 383
QY TTTATTTTTTTT ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
209 CTGTATCCCTGGTGTACATGTGGGCTCTGTGGCAATGTGGTGGATGATCTC 268
Db 384 ATTCGAACAGAGGATCGGACATGTCCACCAACATCTCTCTGTCTGTCCCTGGC 436
QY TTTT ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
269 ATAAATACAGAGGCTCCGAATTATGACCAACATCATCTACCTGTCAACCTGGC 321
RESULT 15
LOCUS N70844 310 bp mRNA EST 14-MAR-1996
DEFINITION za73h08.s1 Homo sapiens cDNA clone 298239 3', similar to gb:M1124
HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(4) ALPHA CHAIN
(HUMAN)).
ACCESSION N70844
NID g1227424
KEYWORDS EST.
SOURCE human clone-298239 primer=ml3 -40 forward library=Soares fetal lung
NHL19W vector=pT73D (Pharmacia) with a modified polylinker
host=DH10B (ampicillin resistant) Rsitel=Not I Rsitel2=Eco RI 19
week fetus. 1st strand cDNA was primed with a Not I - oligo(dT)

primer [5'-TGTTACCAATCTGAAGTGGAGCGCGGCAATTTTTTTTTTTTTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified pT73 vector (Pharmacia). Library went
through one round of normalization to a Cot = 5. Library
constructed by Bento Soares and M.Fatima Bonaldo.
Homo sapiens
ORGANISM
REFERENCE 1 (bases 1 to 310)
AUTHORS Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
Trevaskis E., Waterston R., Williamson A., Wohlmann P. and
Wilson R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
source
1. .310
/organism="Homo sapiens"
/clone="298239"
mRNA
BASE COUNT 71 a 73 c 78 g 63 t 25 others
ORIGIN
Query Match 2.7%; Score 32; DB 19; Length 310;
Best Local Similarity 78.7%; Pred. No. 4.40e-19;
Matches 37; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Db 188 CCNCCACATGCCAGAGGCCACAGNNAACCCCAAGGNGCAGANC 234
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 254 CCACCACATTTGCCAAGAGGCCACAGTGAACACCAACCA3GGAGTACAGC 208
Search completed: Wed Dec 9 01:11:06 1998
Job time : 3150 secs.

WATERMAN

(TM)

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ch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 8 13:11:12 1998; MasPar time 21.71 Seconds
814.247 Million cell updates/sec
Tubular output not generated.

Title: >US-08-963-656-2
Description: (1-355) from US08963656.pep
Perfect Score: 2765
Sequence: 1 MTTSLDTVETFGTTSYDDV.....LERTSSVSPSTAPELSIIVF 355

Scoring table: PAM 150
Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: spiremb6
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 49.326; Variance 131.433; scale 0.375

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1921	69.5	359 11	055169	RECEPTOR PROTEIN CKR3.	9.70e-274
2	1914	69.2	359 11	054814	CHEMOKINE RECEPTOR CCR	1.26e-272
3	1513	54.7	352 6	018770	CCR5 RECEPTOR (FRAGMENT)	4.71e-208
4	1507	54.5	352 6	062745	CHEMOKINE RECEPTOR CCR	4.17e-208
5	1502	54.3	352 6	062744	CHEMOKINE RECEPTOR CCR	2.57e-207
6	1498	54.2	352 6	062746	CHEMOKINE RECEPTOR CCR	1.10e-206
7	1499	54.2	373 11	055193	CHEMOKINE RECEPTOR CCR	7.66e-207
8	1494	54.0	352 4	015538	CCR5 RECEPTOR (FRAGMENT)	4.72e-206
9	1492	54.0	352 6	018771	CCR5 RECEPTOR (FRAGMENT)	9.76e-206
10	1489	53.9	352 6	018772	CCR5 RECEPTOR (FRAGMENT)	2.91e-205
11	1483	53.6	352 6	062743	CHEMOKINE RECEPTOR CCR	2.57e-205
12	1452	52.5	393 14	089609	G PROTEIN-COUPLED RECE	2.01e-199
13	1442	52.2	360 6	018793	CHEMOKINE RECEPTOR.	7.59e-198
14	1375	49.7	333 4	014694	CCR5 RECEPTOR (FRAGMENT)	2.75e-187
15	932	33.7	344 4	000421	CCR6.	4.92e-118
16	877	31.7	384 4	000537	CHEMOKINE RECEPTOR CCR	1.57e-109
17	875	31.6	384 4	000590	CC-CHEMOKINE RECEPTOR	3.19e-109
18	837	30.3	367 11	054689	G PROTEIN-COUPLED RECE	2.30e-103
19	833	30.1	358 13	042444	INTERLEUKIN-8-LIKE REC	9.48e-103
20	815	29.5	378 11	008707	CHEMOKINE (C-C) RECEPT	5.56e-100

21	799	28.9	382 11	009027	CCR10-RELATED RECEPTOR	1.59e-97
22	734	26.5	415 4	035185	G PROTEIN-COUPLED RECE	1.42e-87
23	713	25.8	360 4	060835	CXCR4 GENE ENCODING RE	2.27e-84
24	707	25.6	360 11	070171	L-CCR.	1.86e-83
25	706	25.5	352 6	046428	ALPHA-CHEMOKINE RECEPT	2.65e-83
26	705	25.5	360 11	035457	PUTATIVE BETA CHEMOKIN	3.76e-83
27	693	25.1	352 6	062747	CHEMOKINE RECEPTOR CX	2.52e-81
28	554	20.0	372 11	070526	BRADYKININ B2 RECEPTOR	2.30e-60
29	508	18.4	373 13	057585	OPIOID RECEPTOR HOMOLO	1.60e-53
30	502	18.2	353 13	079960	MESENCHYME-ASSOCIATED	1.23e-52
31	503	18.2	383 13	042324	MU-OPIOID RECEPTOR.	8.77e-52
32	497	18.0	361 11	035811	G-PROTEIN COUPLED RECE	6.77e-52
33	493	17.8	332 11	062973	CHEMOKINE RECEPTOR LCR	2.64e-51
34	490	17.7	381 13	042402	ORNTHOKININ RECEPTOR.	7.31e-51
35	482	17.4	238 13	092158	ANGIOTENSIN II RECEPT	1.11e-49
36	464	16.8	374 13	057466	G PROTEIN COUPLED P2Y	4.89e-47
37	452	16.3	395 11	041666	ANGIOTENSINULIN RECEPT	2.80e-45
38	448	16.2	303 13	070058	ADRENOMEDULLIN RECEPT	1.08e-44
39	449	16.2	375 4	043494	G PROTEIN-COUPLED RECE	7.69e-45
40	433	15.7	404 4	015218	G-PROTEIN COUPLED RECE	1.66e-42
41	431	15.6	345 11	070129	ANAPHYLATOXIN CSA RECE	3.24e-42
42	432	15.6	370 4	015132	P2Y5-LIKE RECEPTOR.	2.32e-42
43	412	14.9	334 11	061125	BRADYKININ RECEPTOR, B	1.85e-39
44	378	13.7	337 11	035782	KININ B1 RECEPTOR.	1.44e-34
45	375	13.6	390 11	034799	NEUROMEDIN B RECEPTOR.	3.87e-34

ALIGNMENTS

RESULT 1
ID 055169 PRELIMINARY; PRT; 359 AA.
AC 055169;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE RECEPTOR PROTEIN CKR3.
OS RATUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE-SPLEEN;
RA HARRINGTON P.M., NEWTON D.J., COLEMAN J.W., FLANAGAN B.F.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; Y13400; E1247073; -.
SQ SEQUENCE 359 AA; 874DF714 CRC32;

Query Match 69.5%; Score 1921; DB 11; Length 359;
Best Local Similarity 68.6%; Pred. No. 9.70e-274;
Matches 242; Conservative 55; Mismatches 53; Indels 3; Gaps 3;

Db	8	LKTVETETPTPEYEWAPP-CEKVSIRELGSWLLPPLYSLVFVIGLLGNMVMVILIKY	66
Qy	5	LDTV-ETGTSY-YDDVGLLCEKADTRALMAQFPVPLYSLVFTFGLGNVVMVILIKY	62
Db	67	RKLQIMTYILLNLALISDLLEFVFWIHYVLMNWFHGMCKMLSGLYLALYSIF	126
Qy	63	RLRLIMTYILLNLALISDLLEFVFWIHYVGRHNVFVHGMCKMLSGFYHTGLYSIF	122
Db	127	FIILLIDRYLAIVHAVLALRARTVFATISITITWGLAVLAALPEFHFSDQNFGLS	186
Qy	123	FIILLIDRYLAIVHAVLALRARTVFATISITITWGLAVLAALPEFHFETEELFE	182
Db	187	CSPRYPEGEEDSKRFHRLNMFGLAPLLIMVTCYSIIKTLRCNPKKKHKAQLIF	246
Qy	183	CSALPDETVTSWRHFHRTVFCVLPLVMAICYGIITLRCPSKKYKAIRLIF	242
Db	247	VMIYFFFTWPTNVLVLLSASFHSTFLETSCQSHLDLMAQVTEVITHCCNPIIYA	306
Qy	243	VIMAYFFFTWPTNVAILLSSVQSIFLNCDCERTKHLDMVLTVEIVASHCCNPIYA	302
Db	307	FVGERFRKHLRFFHURNVAIVLRKYISFLPGKLEKRTSSVSPSTGEQISVVF	359

QY 303 FVGERFRKYLRRHFFRHLMLHGRYIPFLPSEKLERISSVSPSTAEPSELSIVF 355

RESULT 2

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ID 054814 PRELIMINARY; PRT; 359 AA.
AC 054814;
DT 01-JUN-1998 (TREMBREL. 06, CREATED)
DT 01-JUN-1998 (TREMBREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBREL. 06, LAST ANNOTATION UPDATE)
DE CHEMOKINE RECEPTOR CCR5.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=SPLEEN;
RA JIANG Y., SALAFRANCA M.N., ADHIKARI S., XIA Y., FENG L., SONNTAG M.K.,
RA DEFEBRE C.M., PENNELL N.A., STREIT W.J., HARRISON J.K.;
RL J. NEUROIMMUNOL. 0:0-0(1998).
DR EMBL; AF003954; G2897073; -.
SO SEQUENCE 359 AA; 41643 MW; C1FC70CA CRC32;

Query Match 69.2%; Score 1914; DB 11; Length 359;
Best Local Similarity 68.3%; Pred. No. 1, 26e-272;
Matches 241; Conservative 56; Mismatches 53; Indels 3; Gaps 3;

Db 8 LKTVETETTPYEYEWAPP-CEKVSIRELGSWLLPPLSLVFTVGLGNMVMVYLILIKY 66
QY 5 LDTV-ETFGTTSY-YDDVGLCEKADTRALMAQFVPPPLSVFTFGLGNVVMVILIKY 62

Db 67 RKLOIMNIYLLNLAISDLLFLFPWFHIVLWNEVFGHCCKMGLSLYLALYSEIF 126
QY 63 RLRLIMNIYLLNLAISDLLFLFPWFHIVRGNWVFGHCCKMGLSLYLALYSEIF 122

Db 127 FIILLTIDRYLAIVHVALRARTVTFATITSIITWGFVLAALPEFTFHSODNFGDLS 186
QY 123 FIILLTIDRYLAIVHVALRARTVTFVIVSIWGLAVLAALPEFTFETELFEETL 182

Db 187 CSPRYPEGEEDSWKFRHNRNIFGLALPLIMVICYSGIITLLRCPNKKHKAIOIIF 246
QY 183 CSALYPEDTVSWRHFRLRTIFCLVPLLVMAICYTGIIKLLRCPSSKKYKAIRLIF 242

Db 247 VVMVFEFFWTPYNLVLISAFHSFLETSCQSIHLDLQVTEVITHHCCINPIIYA 306
QY 243 VIMAVFFIWPYPYNAVILLYSQILFNCDCERTKHLDLVLMVTEVIAYSHCCMNPVIYA 302

Db 307 FVGERFRKHLRFFHRNVAIVRYISPLPGEKLERISSVSPSTGEQIEISVVF 359
QY 303 FVGERFRKYLRRHFFRHLMLHGRYIPFLPSEKLERISSVSPSTAEPSELSIVF 355

RESULT 3
ID 018770 PRELIMINARY; PRT; 352 AA.
AC 018770;
DT 01-JAN-1998 (TREMBREL. 05, CREATED)
DT 01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBREL. 06, LAST ANNOTATION UPDATE)
DE CCR5 RECEPTOR (FRAGMENT).
GN CCR5.
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MACCR5-140A;
RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
DR EMBL; AF011538; G2305194; -.
FT PFAM; PF00001; 7tm1.
FT NON_TER 352
SQ SEQUENCE 352 AA; 40523 MW; FIC10E99 CRC32;
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Query Match 54.7%; Score 1513; DB 6; Length 352;
Best Local Similarity 55.5%; Pred. No. 4, 71e-209;
Matches 186; Conservative 83; Mismatches 57; Indels 9; Gaps 9;

Db 20 COKINKQIAARLLPPLYSILVFIQFVGNILVLIINCKRLKSMTDIYLLNLAISDLLF 79
QY 24 CEKADTRALMAQFVPPPLYSILVFTFGLGNVVMVILIKYRLRIMNIYLLNLAISDLLF 83

Db 80 LLVPPVWHAHYAAQ-WDFGNTMCOLLTGLYFICGFFSIFFIILLTIDRYLAIVHVALF 138
QY 84 LVTLPEWIHVYRGHNWVFGHCCKLSSGFVHTGLYSEIFFIILLTIDRYLAIVHVALF 143

Db 139 ARTVTFGVTSVITWVAVFASLPGLIIFTRSQREGUHYT-CSSHFPYSQ-YQFWKNFQTL 196
QY 144 ARTVTFGVTSVITWGLAVLAALPEFIYETE-ELFEETLCSALYPEDTVYS-WRHFTL 201

Db 197 KVIILGLVPLLVWVICYSGIILTKLRCRNEKRRHRAVRLIFTIMIVYFLFWAPYINVL 256
QY 202 RMVIFCLVPLLVMAICYTGIIKLLRCPSS-KKYKAIRLIFVIMAVFFIWPYPYNAVIL 260

Db 257 LNTFQEF-FGLNCCSNRLDQAMQVETGLMTHCCINPIIYAFVGEKFRNYLLVFFQKH 315
QY 261 LSSYSQSLFG-NDCERTKHLDLVLMVTEVIAYSHCCMNPVIYAFVGERFRKYLRRHFFHR 319

Db 316 IAKRFCKCCSIFQOEASERASSVYTRSTGEQIEISV 350
QY 320 LLMHLGRYIPFLPSEKLERISSV-SPSTAEPSELSI 353

RESULT 4
ID 062745 PRELIMINARY; PRT; 352 AA.
AC 062745;
DT 01-AUG-1998 (TREMBREL. 07, CREATED)
DT 01-AUG-1998 (TREMBREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBREL. 07, LAST ANNOTATION UPDATE)
DE CHEMOKINE RECEPTOR CCR5.
OS CERCOBUS TORQUATUS ATYIS (RED-CROWNED MANGABEY) (SOOTY MANGABEY).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA CHEN Z., GETTIE A., HO D.D., MARX P.A.;
RL VIROLOGY 0:0-0(1998).
DR EMBL; AF051904; G3135300; -.
SQ SEQUENCE 352 AA; 40460 MW; E6A5AA07 CRC32;

Query Match 54.5%; Score 1507; DB 6; Length 352;
Best Local Similarity 55.2%; Pred. No. 4, 17e-208;
Matches 185; Conservative 85; Mismatches 56; Indels 9; Gaps 9;

Db 20 COKINKQIAARLLPPLYSILVFIQFVGNILVLIINCKRLKSMTDIYLLNLAISDLLF 79
QY 24 CEKADTRALMAQFVPPPLYSILVFTFGLGNVVMVILIKYRLRIMNIYLLNLAISDLLF 83

Db 80 LLVPPVWHAHYAAQ-WDFGNTMCOLLTGLYFICGFFSIFFIILLTIDRYLAIVHVALF 138
QY 84 LVTLPEWIHVYRGHNWVFGHCCKLSSGFVHTGLYSEIFFIILLTIDRYLAIVHVALF 143

Db 139 ARTVTFGVTSVITWVAVFASLPGLIIFTRSQREGUHYT-CSSHFPYSQ-YQFWKNFQTL 196
QY 144 ARTVTFGVTSVITWGLAVLAALPEFIYETE-ELFEETLCSALYPEDTVYS-WRHFTL 201

Db 197 KVIILGLVPLLVWVICYSGIILTKLRCRNEKRRHRAVRLIFTIMIVYFLFWAPYINVL 256
QY 202 RMVIFCLVPLLVMAICYTGIIKLLRCPSS-KKYKAIRLIFVIMAVFFIWPYPYNAVIL 260

Db 257 LNTFQEF-FGLNCCSNRLDQAMQVETGLMTHCCINPIIYAFVGEKFRNYLLVFFQKH 315
QY 261 LSSYSQSLFG-NDCERTKHLDLVLMVTEVIAYSHCCMNPVIYAFVGERFRKYLRRHFFHR 319

Db 316 IAKRFCKCCSIFQOEASERASSVYTRSTGEQIEISV 350
QY 320 LLMHLGRYIPFLPSEKLERISSV-SPSTAEPSELSI 353
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[illegible]

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DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DN CCR5 RECEPTOR (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
DR ENBL; AF011536; G2305190; -.
DR ENBL; AF011536; G2305190; -.
DR ENBL; AF011534; G2305186; -.
DR PFAM; PF00001; 7tm.1.
FT NON_TER 352
SQ SEQUENCE 352 AA; 40552 MW; BLECA8D9 CRC32;

Query Match 54.0%; Score 1494; DB 4; Length 352;
Best Local Similarity 54.3%; Pred. No. 4.72e-206;
Matches 182; Conservative 87; Mismatches 57; Indels 9; Gaps 9;

20 COKINVKQIAARLLPPLYSLVFIQFVGNMVLVILILINCKRLKSMTDIYLLNLAISDLFF 79
24 CEKADTRALMAQFVPPPLYSLVFTGLGNVVVVMILIKYRRLRMTNIYLLNLAISDLFF 83

Db 80 LLTPVFWAHYAAQA-WDFGNTMCOLLTGLYFIFGFSGIFFIILLTIDRYLAIVHAVFALK 138
84 LVTLPFWIHYVRGNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALR 143

Qy 139 ARTVFGVTSVITVWVAVFASLPGIIFTRSQKGLHYT-CSSHFPYSQ-YQFKNFOTL 196
144 ARTVFGVTSVITVWVAVFASLPGIIFTRSQKGLHYT-CSSHFPYSQ-YQFKNFOTL 196

Db 197 KIVILGLVPLLVVICYSGLIKTLRCRNEKRRHRAVRLFTIMIVYFLFWAPYINVL 256
202 RMTFCLVPLLVMAICYTGIIKTLRCPD-KKKYKALRILFVIMAVFFIPTPINVAIL 260

Qy 257 LNTFQEF-FGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFVGEKFRNYLLVFFQKH 315
261 LSSVQSILFG-NDCEKTKHLDLVMVTEVIAYSCHCMNPVIYAFVGERFRKYLRRHFHRH 319
320 LLMHLGRYIPFLPSEKLERTSSV-SPSTAEPELSI 353

RESULT 9 PRELIMINARY; PRT; 352 AA.
OI8771;
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE CCR5 RECEPTOR (FRAGMENT).
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
DR ENBL; AF011541; G2305200; -.
DR PFAM; PF00001; 7tm.1.
FT NON_TER 352
SQ SEQUENCE 352 AA; 40598 MW; A9BF8EDF CRC32;

Query Match 53.9%; Score 1489; DB 6; Length 352;
Best Local Similarity 54.0%; Pred. No. 2.91e-205;
Matches 181; Conservative 88; Mismatches 57; Indels 9; Gaps 9;

20 COKINVKQIAARLLPPLYSLVFIQFVGNMVLVILILINCKRLKSMTDIYLLNLAISDLFF 79
24 CEKADTRALMAQFVPPPLYSLVFTGLGNVVVVMILIKYRRLRMTNIYLLNLAISDLFF 83

Db 80 LLTPVFWAHYAAQA-WDFGNTMCOLLTGLYFIFGFSGIFFIILLTIDRYLAIVHAVFALK 138
84 LVTLPFWIHYVRGNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALR 143

Qy 139 ARTVFGVTSVITVWVAVFASLPGIIFTRSQKGLHYT-CSSHFPYSQ-YQFKNFOTL 196
144 ARTVFGVTSVITVWVAVFASLPGIIFTRSQKGLHYT-CSSHFPYSQ-YQFKNFOTL 196

Db 197 KIVILGLVPLLVVICYSGLIKTLRCRNEKRRHRAVRLFTIMIVYFLFWAPYINVL 256
202 RMTFCLVPLLVMAICYTGIIKTLRCPD-KKKYKALRILFVIMAVFFIPTPINVAIL 260

Qy 257 LNTFQEF-FGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFVGEKFRNYLLVFFQKH 315
261 LSSVQSILFG-NDCEKTKHLDLVMVTEVIAYSCHCMNPVIYAFVGERFRKYLRRHFHRH 319
316 IAKRFCKCSIFQOEAPERASSVYTRSTGQEISV 350
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Db 20 COKINVKQIAARLLPPLYSLVFIQFVGNMVLVILILINCKRLKSMTDIYLLNLAISDLFF 79
24 CEKADTRALMAQFVPPPLYSLVFTGLGNVVVVMILIKYRRLRMTNIYLLNLAISDLFF 83

Db 80 LLTPVFWAHYAAQA-WDFGNTMCOLLTGLYFIFGFSGIFFIILLTIDRYLAIVHAVFALK 138
84 LVTLPFWIHYVRGNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALR 143

Qy 139 ARTVFGVTSVITVWVAVFASLPGIIFTRSQKGLHYT-CSSHFPYSQ-YQFKNFOTL 196
144 ARTVFGVTSVITVWVAVFASLPGIIFTRSQKGLHYT-CSSHFPYSQ-YQFKNFOTL 196

Db 197 KIVILGLVPLLVVICYSGLIKTLRCRNEKRRHRAVRLFTIMIVYFLFWAPYINVL 256
202 RMTFCLVPLLVMAICYTGIIKTLRCPD-KKKYKALRILFVIMAVFFIPTPINVAIL 260

Qy 257 LNTFQEF-FGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFVGEKFRNYLLVFFQKH 315
261 LSSVQSILFG-NDCEKTKHLDLVMVTEVIAYSCHCMNPVIYAFVGERFRKYLRRHFHRH 319
316 IAKRFCKCSIFQOEAPERASSVYTRSTGQEISV 350

RESULT 10 PRELIMINARY; PRT; 352 AA.
OI8772;
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE CCR5 RECEPTOR (FRAGMENT).
OS PAN TROGLODYTES (CHIMPANZEE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RL AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
DR ENBL; AF011541; G2305200; -.
DR PFAM; PF00001; 7tm.1.
FT NON_TER 352
SQ SEQUENCE 352 AA; 40598 MW; A9BF8EDF CRC32;

Query Match 53.9%; Score 1489; DB 6; Length 352;
Best Local Similarity 54.0%; Pred. No. 2.91e-205;
Matches 181; Conservative 88; Mismatches 57; Indels 9; Gaps 9;

20 COKINVKQIAARLLPPLYSLVFIQFVGNMVLVILILINCKRLKSMTDIYLLNLAISDLFF 79
24 CEKADTRALMAQFVPPPLYSLVFTGLGNVVVVMILIKYRRLRMTNIYLLNLAISDLFF 83

Db 80 LLTPVFWAHYAAQA-WDFGNTMCOLLTGLYFIFGFSGIFFIILLTIDRYLAIVHAVFALK 138
84 LVTLPFWIHYVRGNWVFGHGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALR 143

Qy 139 ARTVFGVTSVITVWVAVFASLPGIIFTRSQKGLHYT-CSSHFPYSQ-YQFKNFOTL 196
144 ARTVFGVTSVITVWVAVFASLPGIIFTRSQKGLHYT-CSSHFPYSQ-YQFKNFOTL 196

Db 197 KIVILGLVPLLVVICYSGLIKTLRCRNEKRRHRAVRLFTIMIVYFLFWAPYINVL 256
202 RMTFCLVPLLVMAICYTGIIKTLRCPD-KKKYKALRILFVIMAVFFIPTPINVAIL 260

Qy 257 LNTFQEF-FGLNCCSSNRLDQAMQVETGLMTHCCINPIIYAFVGEKFRNYLLVFFQKH 315
261 LSSVQSILFG-NDCEKTKHLDLVMVTEVIAYSCHCMNPVIYAFVGERFRKYLRRHFHRH 319
316 IAKRFCKCSIFQOEAPERASSVYTRSTGQEISV 350
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QY 252 WTPYNVAILLSSYQSILFG-NDCERT^TKHLDLVMLVTEVIAYSHCCMNPIYAFVGG

Db 315 YLSMFRKVIITRCKQCQVFFREVDGVTSTNTSTABQEV 357
 || ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 311 YLRHFFHRLHLLHGLRPIFLPSEKLE-TRSSVSPSTABPELS 352

RESULT 14
 ID O14694 PRELIMINARY; PRT: 333 AA.
 AC O14694;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE CCR5 RECEPTOR (FRAGMENT).
 GN CCR5.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
 RA HO D.D.;
 RA AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).
 EMBL; AF011504; G2305126; -.
 PFAM; PF00001; 7tm_1.
 FT NON-TER 333
 SQ SEQUENCE 333 AA; 38174 MW; DC2CDIE3 CRC32;

Query Match 49.7%; Score 1375; DB 4; Length 333;
 Best Local Similarity 54.9%; Pred. No. 2.75e-187;
 Matches 169; Conservative 79; Mismatches 51; Indels 9; Gaps 9;
 Db 28 GNMVLILINCKRUKSMTDIYLLNLAISDLFLTLTVFVWAAQ-WDFGNTWCQLLT 86
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 51 GNVVVMILIKYRRLRIMNIYLLNLAISDLFLTLTVFVWAAQ-WDFGNTWCQLLT 110
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 87 GLYFTGFGSIFILLTDRLVAVHAFKATVFGVTSVITWVAVFASLPGII 146
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 111 GFYHGLSEIFILLTDRLVAVHAFKATVFGVTSVITWVAVFASLPGII 170
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 147 FTRSQEGLHYT-CSSHFPYSQ-YOFWKNFQTKVIGLVLPLVWVCYSGIUKTLR 204
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 171 FYETE-ELFEEELSCALYPEDVYS-WRHFTLRWICLVLPLVWVCYSGIUKTLR 228
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 205 CRNEKKRRHRAVLITIMIVFLWAPNIVLLNTFOEF-FGLNNCSSNRDLQAMQVT 263
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 229 CPS-KKKYKAIRLIEVAVFIFWTPYNAVLLSSYSQSLFG-NDCCERTKHLDLVLMVT 286
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 264 ETLGTHCCINPIIYAFVGEKERNVLLVFFQKIAKRCCKCSIFQOEAPERASSVYTR 323
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 287 EVIAYSHCCMNPVIYAFVGERPKYLRHFFHRLHLLHGLRPIFLPSEKLETRSSV-SPS 345
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 324 TGEQFISV 331
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 346 TAEPELSI 353

RESULT 15
 ID O00421 PRELIMINARY; PRT: 344 AA.
 AC O00421;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE CCR6.
 GN CCR6 OR CCRX.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MCCOMBIE W.R., WILSON R., CHEN E., GIBBS R., ZUO L., JOHNSON D.,
 RA NHAN M., PARNELL L., DEDHIA N., ANSARI A., MARDIS E., SCHUTZ K.,
 RA GNOJ L., LA BASTIDE M., KAPLAN N., GRECO T., TOUCHMAN J., MUZYNY D.,
 RA CHEN C.N., EVANS C., FITZGERALD M., SEE L.H., TANG M., PORCEL B.M.,

RA DRAGAN Y., GIACALONE J., PAE A., POWELL E., SOLINSKY K.A., DESTILVA U.,
 RA DIAZ-PEREZ S., ZHOU X., YU Y., WATANABE K., DOGGETT N., GARCIA D.,
 RA SAGRIPANTI J.L.;
 RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA ANSARI-LARI M.A., LIU X.-M., GORRELL J.H., GIBBS R.A.;
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA FAN P., KYAW H., SU K., ZENG Z., AUGUSTUS M., CARTER K.C., LI Y.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 243:264-268(1998).
 DR EMBL; U95626; G2104521; -.
 DR EMBL; AF014958; G2305264; -.
 DR EMBL; U97123; G2897071; -.
 DR PFAM; PF00001; 7tm_1.
 SQ SEQUENCE 344 AA; 39529 MW; C87A6CB5 CRC32;

Query Match 33.7%; Score 932; DB 4; Length 344;
 Best Local Similarity 44.7%; Pred. No. 4.92e-118;
 Matches 134; Conservative 73; Mismatches 76; Indels 17; Gaps 12;
 Db 28 CDKYDAQALSQAQLVPSLCSAVEVIGVLDNLAVLLVLYKGLKRVENIYLLNLAVSNLCF 87
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 24 CEKADTRALMAQFVPPVLSLVFTFGLGNVVVVMILIKYRRLRIMNIYLLNLAISDLFL 83
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 88 LTLTPFWAH-A-G-----GDPMKILIGLYEVGLYSETFFNCLLTQVRYLVFLKHGNEFS 140
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 84 LVTLPFWHYVGRHNVWFGHGMCKLLSGFYHTGLYSEIFFILLTDRLVLAIVH-AVF-A 141
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 141 AR-RRVPGIITSVLAVWTAITLPEYVYKQWEDQYKCAFSPFPLPADETF-WKH 198
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 142 LRARTVTFGVITSITWGLVLAALPEFIY--ETEEL-PEETLCSALY-PEDTVYSWRH 197
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 199 FLTKMNSVLVLPFLFTFLYVQVRKTL-RFRQR-YSEKLVFAIMVFLWAPYNI 256
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 198 FHTLRMTIFCLVLLVMAICYTGIIKTLRCPSKKYKAIRLIFVIMAVFEIFWTPYV 257
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 257 AFFLSTFKEHFSLSCKSSYNLDKSVHITKLIATTECCINPLLAFDGTGSKYLCRCFH 316
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 258 AILLSSYSQILFGNDCERTKHLDLVLMVTEVIAYSHCCMNPVIYAFVGERPKYLRHFFH 317

Search completed: Tue Dec 8 13:12:41 1998
 Job time : 89 secs.

DR EMBL: AF026535: G2582566; -
 DR GCRDB: GCR_0988; -
 DR GCRDB: GCR_1931; -
 DR GCRDB: GCR_1934; -
 DR GCRDB: GCR_1993; -
 DR GCRDB: GCR_1993; -
 DR GCRDB: GCR_2529; -
 DR MIN: 601268; -
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 35 62 1 (POTENTIAL).
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 73 93 2 (POTENTIAL).
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 204 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 FT CONFLICT 276
 SQ SEQUENCE 355 AA; 41043 MW; EB145247 CRC32;

Query Match 99.4%; Score 2748; DB 1; Length 355;
 Best Local Similarity 99.4%; Pred. No. 0.00e+00;
 Matches 353; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MTSLDTVETGTTSSYDDVGLLCEKADTRALMAQVPPVLSVFTVGLGNVVMILI 60
 Qy 1 MTSLDTVETGTTSSYDDVGLLCEKADTRALMAQVPPVLSVFTVGLGNVVMILI 60
 Db 61 KYRRLRIMNTIYLLNLAISDLLFLTPFWHYRGHNWVFGHGCKLLSGFYHTGLYSE 120
 Qy 61 KYRRLRIMNTIYLLNLAISDLLFLTPFWHYRGHNWVFGHGCKLLSGFYHTGLYSE 120
 Db 121 IFFIILLTIDRYLAIVHAFALRARTVTFGVTISVTWGLAVLALPFIETEEELFEE 180
 Qy 121 IFFIILLTIDRYLAIVHAFALRARTVTFGVTISVTWGLAVLALPFIETEEELFEE 180
 Db 181 TLCSALYPEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIIKTLRCPKSKKYKAIRL 240
 Qy 181 TLCSALYPEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIIKTLRCPKSKKYKAIRL 240
 Db 241 IFVIMAVFFIETWPNVAILSSYQSILFGNDCERSKHLDLVLMVTEVIAYSHCCMNPI 300
 Qy 241 IFVIMAVFFIETWPNVAILSSYQSILFGNDCERSKHLDLVLMVTEVIAYSHCCMNPI 300
 Db 301 YAFVGERFKYLRHFFHRLHMLHGRYIPFLPSEKLETSVSPSTAPPELSIVF 355
 Qy 301 YAFVGERFKYLRHFFHRLHMLHGRYIPFLPSEKLETSVSPSTAPPELSIVF 355

RESULT 2
 ID CKR3_CERAE STANDARD; PRT; 355 AA.
 AC P56492;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3).
 GN CMKBR3.
 OS CERCOPTHECUS AETHIOPS (GREEN MONKEY) (GRIVET).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SOL N., TREBOUTE C., GOMAS E., FERCHAL F., ALIZON M.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,

CC MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: Y13775; E1191907; -
 DR GCRDB: GCR_2422; -
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
 KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 35 62 1 (POTENTIAL).
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 73 93 2 (POTENTIAL).
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 204 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 SQ SEQUENCE 355 AA; 40830 MW; AED65DF8 CRC32;

Query Match 91.8%; Score 2539; DB 1; Length 355;
 Best Local Similarity 91.5%; Pred. No. 0.00e+00;
 Matches 325; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Db 1 MTSLYVTEFGPTSYDDMGLLCEKADVGALIAQVPPVLSVFTVGLGNVVMILI 60
 Qy 1 MTSLDTVETGTTSSYDDVGLLCEKADTRALMAQVPPVLSVFTVGLGNVVMILI 60
 Db 61 KYRRLRIMNTIYLLNLAISDLLFLTPFWHYRGHNWVFGHGCKVLSGYHTGLYSE 120
 Qy 61 KYRRLRIMNTIYLLNLAISDLLFLTPFWHYRGHNWVFGHGCKVLSGYHTGLYSE 120
 Db 121 IFFIILLTIDRYLAIVHAFALRARTVTFGVTISVTWGLAVLALPFIETEEELFEE 180
 Qy 121 IFFIILLTIDRYLAIVHAFALRARTVTFGVTISVTWGLAVLALPFIETEEELFEE 180
 Db 181 TLCSALYPEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIIKTLRCPKSKKYKAIRL 240
 Qy 181 TLCSALYPEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIIKTLRCPKSKKYKAIRL 240
 Db 241 IFVIMAVFFIETWPNVAILSSYQSILFGNDCERSKHLDLVLMVTEVIAYSHCCMNPI 300
 Qy 241 IFVIMAVFFIETWPNVAILSSYQSILFGNDCERSKHLDLVLMVTEVIAYSHCCMNPI 300
 Db 301 YAFVGERFKYLRHFFHRLHMLHGRYIPFLPSEKLETSVSPSTAPPELSIVF 355
 Qy 301 YAFVGERFKYLRHFFHRLHMLHGRYIPFLPSEKLETSVSPSTAPPELSIVF 355

RESULT 3
 ID CKR3_MACMU STANDARD; PRT; 355 AA.
 AC P56483;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3).
 GN CMKBR3.
 OS MACACA MULATTA (RHESUS MACAQUE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HAUSER D.A., MARGULIES B.J., CLEMENTS J.E.;
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA SOL N., TREBOUTE C., GOMAS E., FERCHAL F., ALIZON M.;

RP SEQUENCE FROM N.A.
RC SPECIES=M.MULATTA;
RA HAUSER D.A., MARGULIES B.-J., CLEMENTS J.E.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.MULATTA, M.FASCICULARIS, AND M.NEMESTRINA;
RX MEDLINE; 97268687;
RA EDINGER A.L., AMEDEE A., MILLER K., DORANZ B.J., ENDRES M.,
RA SHARRON M., SAMSON M., LU Z.H., CLEMENTS J.E., MURPHY-CORB M.,
RA PEPPER S.C., PARMENTIER M., BRODER C.C., DOMS R.W.;
RL PROC. NATL. ACAD. SCI. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U7672; G1850350; -;
DR EMBL; U73739; G1771981; -;
DR EMBL; U96762; G2088633; -;
DR EMBL; AF005660; G2245614; -;
DR EMBL; AF005661; G2245616; -;
DR EMBL; AF005662; G2245618; -;
DR GCRDB; GCR_1296; -;
DR GCRDB; GCR_1369; -;
DR GCRDB; GCR_1370; -;
DR GCRDB; GCR_1371; -;
DR GCRDB; GCR_1639; -;
DR GCRDB; GCR_1641; -;
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT TRANSMEM 352 352
FT DISULFID 101 178
FT CARBOHYD 268 268
FT CONFLICT 241 241
FT CONFLICT 292 292
SQ SEQUENCE 352 AA; 40507 MW; 9B6826EC CRC32;
Query Match 54.9%; Score 1519; DB 1; Length 352;
Best Local Similarity 55.5%; Pred. No. 1.21e-232;
Matches 186; Conservative 84; Mismatches 56; Indels 9; Gaps 9;
Db 20 COKINVKOIAARLLPPLYSLVFIFGVGNILVLLINCKRLKSMKTDIYLLNLAISDLFF 79
Qy 24 CEKADTRALMAQFPPLYSLVFTGLGNVVMVLLIKYRLRINTNYLLNLAISDLFF 83
Db 80 LLTVPFWAHYAAQ-WDFGNWTCOLLTGLYFGFSGIFFILLTIDRYLAIVHAFALK 138
Qy 84 LVTLPFWHYHVRGNWVFGHGMCKLLSGFYHTGLYSEIFFILLTIDRYLAIVHAFALR 143
Db 139 ARTVTEGVTVITWVAVFASLPGLIITRSQREGLHYT-CSSHFPYSQ-YQFWKNQFTL 196
Qy 144 ARTVTEGVTVITWVAVFASLPGLIITRSQREGLHYT-ELFETLCSALYPEDTVYS-WRHFPTL 201
Db 197 KMWILGLVPLVMVVCYSGIKTLRLCRNEKKRRHVRVLIPTIMVYFLFWAPYNIYLL 256
Qy 202 RMTIFCLVPLVMAICVTGIKTLRLCRPS-KKRYKALRILFVIMAVEFIFWYFNAIL 260

Db 257 LNTQEP-FGLNCCSSNRLDQAMQVTTGLMTHCCNPIIYAFVGEKFRNLYLVFQKH 315
Qy 261 LSSQSLIFG-NDGERTKHLDMVLTVEIVAYSHCCNPNVIYAFVGERFRKYLRRHFRH 319
Db 316 IAKRFCKCSIFQOEAPERASSVYTRSTGEOEISV 350
Qy 320 LMLHGRYIPFLPSEKLERTSSV-SPSTAEPESL 353
RESULT 9
ID CKR5_CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CMKBR5
OS CERCOPIHCEUS AETHIOPS (GREEN MONKEY) (GRIVET).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=KIDNEY;
RX MEDLINE; 98001387.
RA KUHMAN S.E., PLATT E.J., KOZAK S.L., KABAT D.;
RL J. VIROL. 71:8642-8656(1997).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U83324; G2347108; -;
DR EMBL; U83325; G2347110; -;
DR GCRDB; GCR_2465; -;
DR GCRDB; GCR_2466; -;
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; POLYMORPHISM.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT VARIANT 14 14
FT VARIANT 352 352
SQ SEQUENCE 352 AA; 40561 MW; 9CA7E235 CRC32;
Query Match 54.6%; Score 1511; DB 1; Length 352;
Best Local Similarity 55.2%; Pred. No. 3.04e-231;
Matches 186; Conservative 84; Mismatches 58; Indels 9; Gaps 9;
Db 20 COKINVKOIAARLLPPLYSLVFIFGVGNILVLLINCKRLKSMKTDIYLLNLAISDLFF 79
Qy 24 CEKADTRALMAQFPPLYSLVFTGLGNVVMVLLIKYRLRINTNYLLNLAISDLFF 83
Db 80 LLTVPFWAHYAAQ-WDFGNWTCOLLTGLYFGFSGIFFILLTIDRYLAIVHAFALK 138
Qy 84 LVTLPFWHYHVRGNWVFGHGMCKLLSGFYHTGLYSEIFFILLTIDRYLAIVHAFALR 143
Db 139 ARTVTEGVTVITWVAVFASLPGLIITRSQREGLHYT-CSSHFPYSQ-YQFWKNQFTL 196

CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR EMBL: AF005663; G2245620; -

DR EMBL: U94329; G2145188; -

DR EMBL: AF011542; G2305202; -

DR EMBL: U97666; G2327059; -

DR EMBL: AF011540; G2305198; -

DR EMBL: U89797; G2281445; -

DR GCRDB: GCR_1284; -

DR GCRDB: GCR_1367; -

DR GCRDB: GCR_2432; -

DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.

KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.

DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

TRANSMEM 31 58 1 (POTENTIAL).

DOMAIN 59 68 2 (POTENTIAL).

TRANSMEM 69 89 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).

FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 142 166 4 (POTENTIAL).

FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 199 218 5 (POTENTIAL).

FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 236 260 6 (POTENTIAL).

FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 278 301 7 (POTENTIAL).

FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).

FT DSULFID 101 178 BY SIMILARITY.

FT CARBOHYD 268 268 POTENTIAL.

FT CONFLICT 123 123 T -> S (IN REF. 1).

SQ SEQUENCE 352 AA; 40539 MW; D6554684 CRC32;

Query Match 54.2%; Score 1498; DB 1; Length 352;
Best Local Similarity 54.6%; Pred. No. 5,71e-229;
Matches 183; Conservative 87; Mismatches 56; Indels 9; Gaps 9;

Db 20 COKINVOIAARLPPLYSVLFIFGFGVGNMLVILINCKRLKSMTDIYLLNLAISDLFF 79

Qy 24 CEKADTRALMAQFVPLYSVLFTEGLGNVVMILIKYRLRMTYLLNLAISDLFF 83

80 LLTVPFVNAHAAQ-WDFGNMTCOLLGLFIFGFGFIFILLTIDRYLAIVHAFVAK 138

84 LVLPFWIHYVRGHNWVFGHGMCKLLSGFYHTGLSYEIFFILLTIDRYLAIVHAFVAK 143

139 ARTVTFGVTSVITWVAVFASLPGLIFTRSQKGLHYT-CSSHFPYSQ-YQWKNFOTL 196

Qy 144 ARTVTFGVTSVITWVAVFASLPGLIFTRSQKGLHYT-ELFETLCSALYEDTVIS-WRHFHTL 201

197 KIVILGLVPLLVVICYSGLTKLTKCRNEKRRHRAVRLIFTIMVYFLFWAPYNIVLL 256

Qy 202 RMTIFCLVPLLVNAICYTGIIKTLRLCPK-KKKYKAILFVIMAVEFFIWPYNVAIL 260

257 LNTQEP-FGLNCCSNRLDQANQVETLGMTHCCINPIYAFVGEKFRNLLVFFQKH 315

Qy 261 LSSYSQSLFG-NDCKRTKHLDLVNLTEVIAYSHCCMNPVIAFVGERFRKYLHFFHRH 319

316 IAKRFCKCSIFQOEAPERASSVTRSTGGEISV 350

Qy 320 LLMLHGYIFPLPSEKLEKLTSSV-SPSTAEPELSI 353

RESULT 14

ID CKR5_MOUSE STANDARD; PRT: 354 AA.
AC P51682; Q61867; P97405; O35313; P97308; O35891;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (MIP-1
DE ALPHA RECEPTOR).

GN CMKBR5.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=SPLEEN;
RX MEDLINE; 96205938.
RA BORING L., GOSLING J., MONTECLARO F.S., LUSIS A.J., TSOU C.-L.,
RA CHARO I.F.;
RL J. BIOL. CHEM. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=THYMUS;
RX MEDLINE; 96278910.
RA MEYER A., COYLE A.J., PROUDFOOT A.E.I., WELLS T.N.C., POWER C.A.;
RL J. BIOL. CHEM. 271:14445-14451(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/OLA;
RA KUZIEL W.A., BECK M.A., DANSON T.C., MAEDA N.;
RL SUBMITTED (DEC-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6. AND NIH/SWISS; TISSUE=LIVER, KIDNEY, AND SPLEEN;
RX MEDLINE; 98001387.
RA KOHMANN S.E., PLATT E.J., KOZAK S.L., KABAT D.;
RL J. VIROL. 71:8642-8656(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE; 97404635.
RA DORANZ B.J., LU Z.H., RUCKER J., ZHANG T.Y., SHARRON M., CEN Y.H.,
RA WANG Z.X., GUO H.H., DU J.G., ACCAVITTI M.A., DOMS R.W., PEIPER S.C.;
RL J. VIROL. 71:6305-6314(1997).
RN [6]
RP SEQUENCE FROM N.A.
GUO B., KUNO K., HARADA A., MATSUSHIMA K.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
BUT NOT IN NONHEMATOPOIETIC CELL LINES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: U47036; G1237136; -
DR EMBL: X94151; E218395; -
DR EMBL: U68565; G1698716; -
DR EMBL: U83327; G2347114; -
DR EMBL: AF022990; G2444487; -
DR EMBL: AF019772; G2431976; -
DR EMBL: D83648; G1777330; -
DR GCRDB: GCR_1150; -
DR GCRDB: GCR_1645; -
DR GCRDB: GCR_1656; -
DR GCRDB: GCR_1729; -
DR GCRDB: GCR_2449; -
DR GCRDB: GCR_2540; -
DR GCRDB: GCR_2554; -
DR MGD; MGI:107182; CMKBR5.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; POLYMORPHISM.
FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 33 60 1 (POTENTIAL).
FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 91 2 (POTENTIAL).
FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 105 126 3 (POTENTIAL).
FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 144 168 4 (POTENTIAL).
FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 201 220 5 (POTENTIAL).

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FT DOMAIN 221 237
FT TRANSMEM 238 262
FT DOMAIN 239 279
FT TRANSMEM 280 303
FT DOMAIN 304 354
FT DISULFID 103 180
FT CARBOHYD 270 270
FT VARIANT 11 11
FT VARIANT 62 62
FT VARIANT 66 66
FT VARIANT 97 97
FT VARIANT 109 109
FT VARIANT 156 156
FT VARIANT 160 160
FT VARIANT 185 185
FT VARIANT 213 213
FT VARIANT 318 318
FT VARIANT 337 337
FT CONFLICT 3 3
FT CONFLICT 80 80
FT CONFLICT 190 190
FT CONFLICT 208 208
FT CONFLICT 145 145
FT CONFLICT 145 145
SEQUENCE 354 AA; 40863 MW; 6ECD306A CRC32;

Query Match 54.2%; Score 1500; DB 1; Length 354;
Best Local Similarity 54.4%; Pred. No. 2,556-229;
Matches 181; Conservative 83; Mismatches 62; Indels 7; Gaps 7;

Db 22 COKINKVQAOLPLPLSLVIFGFGNMVFLILISCKLKSVTDIYLLNLAISDLFL 81
QY 24 CEKADTRALMAQFVPLSLVIFGFGNMVFLILISCKLKSVTDIYLLNLAISDLFL 83
Db 82 LITLPEWHAHA-ANEMIFGNMCKVFTGYHGGIFFIILLTIDRYLAIVHAFVALK 140
QY 84 LVTLPWIHVHGNVWFGHGMCKLSGYHTGLYSEIFFIILLTIDRYLAIVHAFVLR 143
Db 141 VRTVNEGVITSVTVWVAVFASLPELIFTRSKQEGFHT-CSPHPHTQYHFWKSFOLK 199
QY 144 ARTVFGVITSVTVWVAVFASLPELIFTRSKQEGFHT-CSPHPHTQYHFWKSFOLK 202
Db 200 MWLSLILPLLVMIICYSGILHTFCRNEKRRHRAVRLIFAIMIVYFLFWTPYNNVILL 259
QY 203 MTIFCLVPLLVMAICYTGIIITLRCPS-KKYYKAIRLIFVIMAVFFIFTWPNVAILL 261
Db 260 TTFQEF-FGLNCCSSNRDLQAMQATETLGMTHCCCLNPNVYAFVGEKFSYLSVFRKHI 318
QY 262 SSVQSILFG-NDCCRTKHLDLVMLVTEVYASHCCMNPVYAFVGERFRKYLHFFHRL 320
Db 319 VRFCKRCSIFQODPNDRVSSVYTRSTGHEVS 351
QY 321 LMHLGRYIPFLPSEKLERTSSV-SPSTARPELS 352

RESULT 15
ID CKRS_HUMAN STANDARD; PRT; 352 AA.
AC P51681; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5)
DE (HIV-1 FUSION CO-RECEPTOR) (CHEMR13).
GN CMKRS.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96241590.
RA SAMSON M., LABBE O., MOLLEREAU C., VASSART G., PARMENTIER M.;
RL BIOCHEMISTRY 35:3362-3367(1996).
RN [2]
RP SEQUENCE FROM N.A.
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RX MEDLINE; 96291862.
RA RAPORT C.J., GOSLING J., SCHWEICHAERT V.L., GRAY P.W., CHARO I.F.;
RL J. BIOL. CHEM. 271:17161-17166(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96295970.
RA COMBADIERE C., AHUJA S.K., TIFFANY H.L., MURPHY P.M.;
RL J. LEUKOC. BIOL. 60:147-152(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA MCCOMBIE W.R., WILSON R., CHEN E., GIBBS R., ZUO L., JOHNSON D.,
RA NHAN M., PARNELL L., DEDHIA N., ANSARI A., MARDIS E., SCHUTZ K.,
RA GNOI L., LA BASTIDE M., KAPLAN N., GRECO T., TOUCHMAN J., TANG M.,
RA MUZY D., CHEN C.N., EVANS C., FITZGERALD M., SEE L.H., POWELL E.,
RA PORCEL B.M., DRAGAN Y., GIACALONE J., PAE A., POWELL E.,
RA SOLINSKY K.A., DESILVA U., DIAZ-PEREZ S., ZHOU X., YU Y.,
RA WATANABE M., DOGGETT N., GARCIA D., SAGRIPANTINI J.L.;
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98001387.
RA KUHMAN S.E., PLATT E.J., KOZAK S.L., KABAT D.;
RL J. VIROL. 71:8642-8656(1997).
RN [6]
RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX MEDLINE; 98022612.
RA ZHANG L., CARRUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RL AIDS RES. HUM. RETROVIRUSES 13:1357-1366(1997).
RN [7]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE; 96260017.
RA DENG H., LIU R., ELLMEIER W., CHOE S., UNUTMAZ D., BURKHART M.,
RA DI MARZIO P., MARZIO S., SUTTON R.E., HILL C.M., DAVIS C.B.,
RA PEIPER S.C., SCHALL T.J., LITTMAN D.R., LANDAU N.R.;
RL NATURE 381:661-666(1996).
RN [8]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE; 96260018.
RA DRAGIC T., LITWIN V., ALLAWAY G.P., MARTIN S.R., HUANG Y.,
RA NAGASHIMA K.A., CAVANAN C., MADDON P.J., KOUP R.A., MOORE J.P.,
RA PAXTON W.A.;
RL NATURE 381:667-673(1996).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -!- FUNCTION: ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
CC SYNCYTUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1
CC VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; X91492; E199247; -
DR EMBL; U54994; G1457946; -
DR EMBL; U57840; G1502409; -
DR EMBL; U95626; G2104520; -
DR EMBL; U83326; G2347112; -
DR EMBL; AF011500; G2305118; -
DR EMBL; AF011501; G2305120; -
DR EMBL; AF011502; G2305122; -
DR EMBL; AF011503; G2305124; -
DR EMBL; AF011505; G2305128; -
DR EMBL; AF011506; G2305130; -
DR EMBL; AF011507; G2305132; -
DR EMBL; AF011508; G2305134; -
DR EMBL; AF011509; G2305136; -
DR EMBL; AF011510; G2305138; -
DR EMBL; AF011511; G2305140; -
DR EMBL; AF011512; G2305142; -
DR EMBL; AF011513; G2305144; -
DR EMBL; AF011514; G2305146; -
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WQSELEH (TM)

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ch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 8 13:19:33 1998; MasPar time 11.52 Seconds
Tabular output not generated. 498.610 Million cell updates/sec

Title: >US-08-963-656-4
Description: (1-355) from US08963656.pep
Perfect Score: 2760
Sequence: 1 MTTSLDVTVEFTGTSYDDV.....LERTSSVSPSTAEPSELSIVF 355

Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 34.811; Variance 169.172; scale 0.206

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	2760	100.0	355	28	Human eosinophil eota	2.88e-228
2	2760	100.0	355	24	Human chemokine recep	2.88e-228
3	2760	100.0	355	19	CC-chemokine receptor	2.88e-228
4	2758	99.9	355	23	Human C-C chemokine r	4.32e-228
5	2758	99.9	355	19	CC-chemokine receptor	4.32e-228
6	2722	98.6	355	26	Human CCR3 chemokine	6.57e-225
7	2668	96.7	355	19	CC-chemokine receptor	3.89e-220
8	1834	66.4	355	11	Human MIP-1 alpha/RAN	1.32e-146
9	1834	66.4	355	25	Human MIP-1 alpha/RAN	1.32e-146
10	1834	66.4	355	24	Rat CC chemokine rece	4.07e-137
11	1726	62.5	355	24	Macaque chemokine rec	4.95e-117
12	1497	54.2	352	24	Human chemokine recep	6.81e-116
13	1484	53.8	352	27	Human CCR5	6.81e-116
14	1484	53.8	352	29	Human CC chemokine re	5.57e-116
15	1485	53.8	371	29	Human G-protein chemo	9.37e-115
16	1471	53.3	352	20	Human monocyte chemoa	2.23e-110
17	1471	53.3	352	20	Human monocyte chemoa	2.23e-110
18	1421	51.5	360	14	Human monocyte chemoa	2.23e-110

19	1421	51.5	360	26	W35833	Human monocyte chemoa	2.23e-110
20	1378	49.9	332	28	W26766	Human chemokine recep	1.28e-106
21	1335	48.4	374	14	R79165	Human monocyte chemoa	7.35e-103
22	1238	44.9	360	19	R99274	Chemokine receptor K5	2.16e-94
23	1067	38.7	355	20	W07618	Human G-protein recep	1.66e-79
24	1011	36.6	355	11	R53748	Seven transmembrane r	1.20e-74
25	940	34.1	356	29	W48087	Human macrophage/dend	1.70e-68
26	927	33.6	344	28	W26767	Human chemokine recep	2.27e-67
27	825	29.9	358	11	R53745	Partial sequence of s	1.45e-58
28	825	29.9	410	11	R53743	Putative seven transm	1.45e-58
29	822	29.8	378	11	R53744	Human dendritic cell	2.63e-58
30	794	28.8	365	29	W48086	Human dendritic cell	6.76e-56
31	796	28.8	378	10	R54079	Epstein Barr virus in	4.55e-56
32	790	28.6	184	27	W27406	Inactive human CCR5	1.49e-55
33	790	28.6	215	27	W27408	Inactive human CCR5	1.49e-55
34	765	27.7	359	11	R53747	Seven transmembrane r	2.10e-53
35	739	26.8	355	7	R33420	Human IL-8 receptor f	3.58e-51
36	739	26.8	360	15	R80758	Interleukin 8 recepto	3.58e-51
37	739	26.8	360	6	R28273	Sequence in a low aff	3.58e-51
38	739	26.8	1064	14	R70124	IL8-R type 2-GFP 130	3.58e-51
39	725	26.3	350	15	R80951	Recombinant high affi	5.68e-50
40	725	26.3	350	12	R68811	Interleukin-8 recepto	5.68e-50
41	725	26.3	350	15	R80756	Interleukin 8 recepto	5.68e-50
42	725	26.3	415	23	W19780	Human G-protein chemo	5.68e-50
43	725	26.3	1060	14	R70123	IL8-R type 1-GFP 130	5.68e-50
44	719	26.1	352	12	R68812	Human monocyte PF4AR	1.85e-49
45	721	26.1	360	15	R80953	Recombinant high affi	1.25e-49

ALIGNMENTS

RESULT 1
ID W31850 standard; Protein; 355 AA.
AC W31850;

DT 07-MAY-1998 (first entry)

DE Human eosinophil eotaxin receptor protein CC CCR3.

KW Eosinophil eotaxin receptor; CC CCR3; human; treatment; dermatitis;

KW atopic condition; allergic rhinitis; conjunctivitis; bronchial asthma;

OS beta-chemokine receptor; viral infection.

OS Homo sapiens.

PN WO9741154-A1.

PN 06-NOV-1997.

PF 24-APR-1997; U065568.

PR 17-JAN-1997; GB-000994.

PR 26-APR-1996; US-016158.

PR 26-APR-1996; US-017113.

PA (MERI) MERCK & CO INC.

PI Daugherty BL, Demartino JA, Siciliano SJ, Springer MS;

DR WPI: 97-549685/50.

DR N-PSDB; T93601.

PT New isolated human eosinophil eotaxin receptor - used to develop

PT products for treating and preventing atopic conditions e.g. allergic

PT rhinitis, dermatitis, conjunctivitis and bronchial asthma

PS Claim 5; Page 15; 51pp; English.

CC This is a human eosinophil eotaxin receptor. The 5099 base pair encoding

CC cDNA sequence comprises a 1065 base pair open reading frame encoding this

CC 355 amino acid eosinophil eotaxin receptor protein, flanked by a 5'

CC genomic DNA sequence and a 3' terminator region. This novel eosinophil

CC eotaxin receptor is a human beta-chemokine receptor designated CC CCR3.

CC Agents which bind to this eosinophil eotaxin receptor can be used for

CC the treatment and prevention of atopic conditions such as allergic

CC rhinitis, dermatitis, conjunctivitis and bronchial asthma. Agents which

CC block this eosinophil eotaxin receptor can be used to prevent viral

CC infection in healthy individuals and slow or halt viral progression

CC in infected patients.

SQ Sequence 355 AA;

Query Match 100.0%; Score 2760; DB 28; Length 355;

Best Local Similarity 100.0%; Pred. No. 2.88e-228;

Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mttsltdvtvetgtsydvvgllceakdralmagfvppylsvlftvgllgnvvwmlii 60

|||||

QY 1 MTTSLDTVETGTTSSYYDDVGLLCEKADTRALMAQFVPLLSLVFTVGLGNVVMVMI 60
 Db 61 KYRRLRIMTNIYLLNLAISDLLFLVLPFWIHYVGRHNWFGHGMCKLLSGFYHTGLYSE 120
 QY 61 KYRRLRIMTNIYLLNLAISDLLFLVLPFWIHYVGRHNWFGHGMCKLLSGFYHTGLYSE 120
 Db 121 IFFIILLIDRYLAIVHAVFALRARTVFGVITSIVTWGLAVLAALPEFIYETEELFEE 180
 QY 121 IFFIILLIDRYLAIVHAVFALRARTVFGVITSIVTWGLAVLAALPEFIYETEELFEE 180
 Db 181 TLCALYPEDTVYSWRHFHTLMTIFCLVPLVMAICYTGIIKTLRCPSKKYKAIRL 240
 QY 181 TLCALYPEDTVYSWRHFHTLMTIFCLVPLVMAICYTGIIKTLRCPSKKYKAIRL 240
 Db 241 IFVIMAVFFIETWPYNVAILSSYSQILFGNDCERSKHLDLVMLVTEVIAYSHCCMPVI 300
 QY 241 IFVIMAVFFIETWPYNVAILSSYSQILFGNDCERSKHLDLVMLVTEVIAYSHCCMPVI 300
 Db 301 YAFVGERFRKYLRHFFHRLHMLGRYIPFLPSEKLETSVSPSTAEPELSIVF 355
 QY 301 YAFVGERFRKYLRHFFHRLHMLGRYIPFLPSEKLETSVSPSTAEPELSIVF 355

LT 2
 ID W27124 standard; Protein; 355 AA.
 AC W27124;
 DE 14-DEC-1997 (first entry)
 DT Human chemokine receptor 88-2B.
 DE Chemokine receptor 88-2B; atherosclerosis; rheumatoid arthritis;
 KW tumour; asthma; viral infection; AIDS; inflammation;
 KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
 KW G protein coupled receptor; ligand; modulator; antibody; human.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT domain 1..36
 FT /label= Extracellular_domain
 FT domain 60..71
 FT /label= Intracellular_domain
 FT domain 93..107
 FT /label= Extracellular_domain
 FT domain 131..151
 FT /label= Extracellular_domain
 FT domain 171..196
 FT /label= Extracellular_domain
 FT domain 219..240
 FT /label= Intracellular_domain
 FT domain 263..284
 FT /label= Extracellular_domain
 FT domain 306..355
 FT /label= Intracellular_domain

WO9722698-A2.
 26-JUN-1997.
 PF 26-DEC-1996; U20759.
 PR 07-JUN-1996; US-661393.
 PR 20-DEC-1995; US-575967.
 PA (ICOS-) ICOS CORP.
 PI Gray PW, Raport CJ, Schweickart VL;
 DR WPI: 97-341689/31.
 DR N-PSDB: T85162.
 PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used
 FT to modulate leukocyte trafficking, e.g. for treatment of
 FT inflammation, tumours, viral infections, autoimmune diseases, etc.
 PS Claim 1; Page 50-51; 65pp; English.
 CC This polypeptide sequence comprises novel human chemokine receptor
 CC 88-2B, a G protein coupled receptor that is involved in leukocyte
 CC trafficking. Its amino sequence was deduced from a cDNA clone
 CC (T85162) isolated from a macrophage library. It shows 72% identity
 CC to CCR1. Chemokine receptor 88C (see W27123) has also been
 CC identified. 88C and 88-2B receptors and their polypeptide fragments
 CC can be produced in transformed host cells. The receptors, peptides
 CC comprising one or more of the extracellular or intracellular
 CC domains, and anti-receptor antibodies can be used to modulate
 CC receptor activities, particularly ligand and G protein binding, and

CC are potentially potentially useful in the treatment of
 CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune
 CC response, abnormal haematopoietic processes etc.
 SQ Sequence 355 AA;
 Query Match 100.0%; Score 2760; DB 24; Length 355;
 Best Local Similarity 100.0%; Pred. No. 2.88e-228;
 Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MTTSLDTVETGTTSSYYDDVGLLCEKADTRALMAQFVPLLSLVFTVGLGNVVMVMI 60
 QY 1 MTTSLDTVETGTTSSYYDDVGLLCEKADTRALMAQFVPLLSLVFTVGLGNVVMVMI 60
 Db 61 KYRRLRIMTNIYLLNLAISDLLFLVLPFWIHYVGRHNWFGHGMCKLLSGFYHTGLYSE 120
 QY 61 KYRRLRIMTNIYLLNLAISDLLFLVLPFWIHYVGRHNWFGHGMCKLLSGFYHTGLYSE 120
 Db 121 IFFIILLIDRYLAIVHAVFALRARTVFGVITSIVTWGLAVLAALPEFIYETEELFEE 180
 QY 121 IFFIILLIDRYLAIVHAVFALRARTVFGVITSIVTWGLAVLAALPEFIYETEELFEE 180
 Db 181 TLCALYPEDTVYSWRHFHTLMTIFCLVPLVMAICYTGIIKTLRCPSKKYKAIRL 240
 QY 181 TLCALYPEDTVYSWRHFHTLMTIFCLVPLVMAICYTGIIKTLRCPSKKYKAIRL 240
 Db 241 IFVIMAVFFIETWPYNVAILSSYSQILFGNDCERSKHLDLVMLVTEVIAYSHCCMPVI 300
 QY 241 IFVIMAVFFIETWPYNVAILSSYSQILFGNDCERSKHLDLVMLVTEVIAYSHCCMPVI 300
 Db 301 YAFVGERFRKYLRHFFHRLHMLGRYIPFLPSEKLETSVSPSTAEPELSIVF 355
 QY 301 YAFVGERFRKYLRHFFHRLHMLGRYIPFLPSEKLETSVSPSTAEPELSIVF 355

RESULT 3
 ID W03377 standard; Protein; 355 AA.
 AC W03377;
 DT 15-NOV-1996 (first entry)
 DE CC-chemokine receptor 3
 DE CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;
 KW antiinflammatory; eosinophil.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT region 130..138
 FT /note= "amino acids 130-138 comprise a motif
 FT conserved among C-X-C and C-C chemokine
 FT receptors".
 PN WO9622371-A2.
 PD 25-JUL-1996.
 PR 19-JAN-1995; U00608.
 PR 19-JAN-1995; US-375199.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 PA (LEUK-) LEUKOSITE INC.
 PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
 DR WPI: 96-354528/35.
 DR N-PSDB: T31335.
 PT Mammalian chemokine receptor-3 and related nucleic acids - useful to
 PT identify receptor inhibitors to treat inflammatory disease, e.g.
 PT autoimmune disorders, certain cancers, etc.
 PS Claim 10; Page 113-114; 153pp; English.
 CC A novel human receptor (W03377), designated Eos L2 or C-C chemokine
 CC receptor 3 (CKR-3), is involved in leukocyte migration associated
 CC with inflammation. Its sequence was deduced from a cDNA clone
 CC (T31335) isolated from a hyper-eosinophilic syndrome patient. A
 CC slightly different amino acid sequence (W03376) was deduced from a
 CC genomic clone (T31334) and a consensus sequence is given in W03378.
 CC Recombinant CKR-3 can be produced in host cells, and is useful for
 CC screening for CKR-3 ligands, promoters and inhibitors. The
 CC inhibitors can be used to treat inflammatory disease.
 SQ Sequence 355 AA;

Query Match 100.0%; Score 2760; DB 19; Length 355;
Best Local Similarity 100.0%; Pred. No. 2.88e-228;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mtsldtvetftgtsydvddgvlckadtralmagfvpplyslvfvgllgnvnmvmlil 60
QY 1 MTSLSDTVETFTGTSYDVDDGVLCKADTRALMAQFVPPLYSLVFTVGLGNVNMVMI 60

Db 61 kyrirrimtniylalnaisdlfivtlpfiwhvgrhnmwvfhgmkllsgfyhtglyse 120
QY 61 KYRRLRIMTNIYLLNLAISDLLFLVTLPEWIVHVRGNWVFGHGMCKLLSGFYHTGLYSE 120

Db 121 iffiilltldrylaivhavfalrartvtfgvitsvltwglavlaalpefifeteelfee 180
QY 121 IFIILLTIDRYLAIVHAVFALRARTVTFGVITSVLTWGLAVLAALPEFIFETEELFEE 180

Db 181 tlcsalypedtvyswrhftlmtfclvplllvmaicygtiiktllrcpskkkykairl 240
QY 181 TLCSALYPEDTVYSWRHFTRLMTFCLVPLLLVMAICYGTIIKTLRLCPSKKYKAIRL 240

Db 241 ifvimavffwtpynvnaillssyqilfgndcerskhldlvmvltvteiayspshccmnpvi 300
QY 241 IFVIMAVFFWTPYNVNAILLSSYQILFGNDCERSKHLDLVMTVEVIAYSHCCMNPVI 300

Db 301 yafvgerfkylrhffrhlmlhgrlyipflpseklertssvstaepelsivf 355
QY 301 YAFVGERFRKYLRFHFRHLMLHGRYIPFLPSEKLERTSVSSPSTAEPELSIVF 355

RESULT 4

ID W10100 standard; Protein: 355 AA.

AC W10100;

DE 30-SEP-1997 (first entry)

DE Human C-C chemokine receptor 3.

KW Human; eotaxin; eosinophil; chemoattractant; stimulation;

KW accumulation; attraction; chemotaxis; diagnosis; prevention;

KW treatment; disease; inflammation; allergy; asthma; rhinitis;

KW hypersensitivity; lung; pneumonia; Loeffler's; syndrome;

KW interstitial; ILD; idiopathic pulmonary fibrosis;

KW rheumatoid arthritis; systemic; lupus erythematosus; SLE;

KW ankylosing spondylitis; sclerosis; Sjorgen's; polymyositis;

KW dermatomyositis; bowel; anaphylaxis; drug; penicillin;

KW cephalosporin; insect sting; Crohn's; ulcerative colitis;

KW spondyloarthropathy; scleroderma; psoriasis; dermatosis;

KW vasculitis; myositis; fascitis; urticaria; necrotizing; cutaneous;

KW myasthenia gravis; juvenile onset diabetes; glomerulonephritis;

KW autoimmune; thyroiditis; Bechet's; graft; rejection;

KW transplantation; allograft; graft versus host; cancer;

KW leukocyte infiltration; reperfusion injury; atherosclerosis;

KW haematologic malignancy; septic; endotoxigenic; shock;

KW polymyositis; dermatomyositis; immunosuppression; immunodeficiency;

KW AIDS; radiation therapy; chemotherapy; autoimmune; corticosteroid;

KW C-C chemokine receptor 3; CRK3.

OS Homo sapiens.

PN MO9700960-A1.

PN 09-JAN-1997.

PF 21-JUN-1996; U10723.

PR 23-JUN-1995; US-494093.

PA (LEUK-) LEUKOSTE INC.

PI Mackay C, Newman W, Ponath PD, Qin S, Ringler DJ;

DR WPI: 97-087387/08.

DR N-PSDB; T58783.

PT New isolated human eotaxin gene - used to develop prods. for the

PT diagnosis and treatment of e.g. inflammation, allergies, auto-immune

PT disease, infections and tumours

PS Example 7; Pages 98-99; 130pp; English.

CC The present sequence is human C-C chemokine receptor 3 (CRK3),

CC to which human eotaxin (hE), an eosinophil specific chemoattractant

CC capable of stimulating eosinophil accumulation and/or attracting

CC eosinophils (including chemotaxis), binds.

CC hE can be used to develop products for the diagnosis, prevention or

treatment of hE associated diseases or conditions. The products can
be used to treat inflammatory or allergic diseases and conditions,
including respiratory allergic diseases (e.g. asthma, allergic
rhinitis, hypersensitivity lung diseases or pneumonitis,
eosinophilic pneumonia, interstitial lung diseases (ILD) and chronic
eosinophilic pneumonia, such as Loeffler's syndrome and chronic
idiopathic pulmonary fibrosis or ILD associated with rheumatoid
arthritis, systemic lupus erythematosus (SLE), ankylosing
spondylitis, systemic sclerosis, Sjorgen's syndrome, polymyositis
or dermatomyositis), systemic anaphylaxis or hypersensitivity
responses, drug allergies (e.g. to penicillin and cephalosporins),
insect sting allergies, inflammatory bowel diseases (e.g. Crohn's
disease and ulcerative colitis), spondyloarthropathies,
scleroderma, psoriasis and inflammatory dermatoses (e.g.
dermatitis, eczema, atopic dermatitis, allergic contact dermatitis,
urticaria and necrotizing, cutaneous and hypersensitivity
vasculitis), eosinophilic myositis and fascitis, multiple
sclerosis, SLE, myasthenia gravis, juvenile onset diabetes,
glomerulonephritis, autoimmune thyroiditis, Bechet's disease, graft
rejection (e.g. in transplantation) including allograft rejection or
graft versus host disease and cancers with leukocyte infiltration
of the skin or organs. The products can also be used to treat other
diseases or conditions requiring the inhibition of undesirable
inflammatory responses, including reperfusion injury.

CC atherosclerosis, certain haematologic malignancies, cytokine
induced toxicity (e.g. septic or endotoxic shock), polymyositis,
dermatomyositis, immunosuppression (e.g. in individuals with
immunodeficiency syndromes such as AIDS, undergoing radiation
therapy, chemotherapy, therapy for autoimmune disease or other drug
therapy, such as corticosteroid therapy, which causes
immunosuppression), immunosuppression due to (e.g. congenital)
deficiency (e.g. in eotaxin) or infectious diseases such as parasitic
diseases.

CC Degenerate primers based on the guinea pig eotaxin amino acid
sequence were used for the reverse transcriptase polymerase chain
reaction (RT-PCR) amplification of RNA isolated from inflamed,
eosinophilic lung tissue obtained from Balb/c mice sensitised to
ovalbumin. The amplification product was used as a probe to screen
a human genomic library in vector EMBL3 SP6/T7 to obtain the hE
gene.

SQ Sequence 355 AA;

Query Match 99.9%; Score 2758; DB 23; Length 355;
Best Local Similarity 99.7%; Pred. No. 4.32e-228;
Matches 354; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 mtsldtvetftgtsydvddgvlckadtralmagfvpplyslvfvgllgnvnmvmlil 60
QY 1 MTSLSDTVETFTGTSYDVDDGVLCKADTRALMAQFVPPLYSLVFTVGLGNVNMVMI 60

Db 61 kyrirrimtniylalnaisdlfivtlpfiwhvgrhnmwvfhgmkllsgfyhtglyse 120
QY 61 KYRRLRIMTNIYLLNLAISDLLFLVTLPEWIVHVRGNWVFGHGMCKLLSGFYHTGLYSE 120

Db 121 iffiilltldrylaivhavfalrartvtfgvitsvltwglavlaalpefifeteelfee 180
QY 121 IFIILLTIDRYLAIVHAVFALRARTVTFGVITSVLTWGLAVLAALPEFIFETEELFEE 180

Db 181 tlcsalypedtvyswrhftlmtfclvplllvmaicygtiiktllrcpskkkykairl 240
QY 181 TLCSALYPEDTVYSWRHFTRLMTFCLVPLLLVMAICYGTIIKTLRLCPSKKYKAIRL 240

Db 241 ifvimavffwtpynvnaillssyqilfgndcerskhldlvmvltvteiayspshccmnpvi 300
QY 241 IFVIMAVFFWTPYNVNAILLSSYQILFGNDCERSKHLDLVMTVEVIAYSHCCMNPVI 300

Db 301 yafvgerfkylrhffrhlmlhgrlyipflpseklertssvstaepelsivf 355
QY 301 YAFVGERFRKYLRFHFRHLMLHGRYIPFLPSEKLERTSVSSPSTAEPELSIVF 355

RESULT 5

ID W03376 standard; Protein: 355 AA.


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Db 59 lvqykrknmtsiylnlaisdlflftlplfwidylkddwvfgdamckllsgfytygly 118
Qy 59 LIKVRRLRIMTNIYLLNLAISDLFLVLPFWIHVVRGHNWVFGHGMCKLLSGFYHTGLY 118
Db 119 seiffilltdrylaihvafalrartvtfgvitsiilwalaalampglyfsktqgef 178
Qy 119 SEIFFIILLTDRLYLAIHVAFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELF 178
Db 179 thtcsfhphesirewklfgalnlgvlplvlmicytgikillrrpnekkaskav 238
Qy 179 EETLCSALYPEDTVYSWRHFHTLMTIFCLVPLLVMAICYTGIIKTLRCPSSKKYKAI 238
Db 239 rlifvimiiflftwpyntllisvfdqflfthceqsrhldlavqvtviaythccvnp 298
Qy 239 RLIFVIMAVFFIWTPTYNVAILLSYOSILFGNDCERSKHLDLVNLVTEVAYSHCCMNP 298
Db 299 viyafvgerfrkylrqlfhrvavhlvkwplfslvdrsvstspstgehelsagf 355
Qy 299 VIYAFVGERFRKYLHRHFHRLHMLGRIYIFLPSEKLERISSTSSVSPSTAPPELSIVF 355
Db 239 rlifvimiiflftwpyntllisvfdqflfthceqsrhldlavqvtviaythccvnp 298
Qy 239 RLIFVIMAVFFIWTPTYNVAILLSYOSILFGNDCERSKHLDLVNLVTEVAYSHCCMNP 298
Db 299 viyafvgerfrkylrqlfhrvavhlvkwplfslvdrsvstspstgehelsagf 355
Qy 299 VIYAFVGERFRKYLHRHFHRLHMLGRIYIFLPSEKLERISSTSSVSPSTAPPELSIVF 355
RESULT 10
W25751 standard; Protein; 355 AA.
W25751;
20-NOV-1997 (first entry)
DE Human MIP-1alpha/RANTES receptor protein.
KW Human MIP-1 alpha/RANTES receptor; osteoporosis; pCCR; digestive ulcer;
KW macrophage inflammatory protein 1 alpha; diabetes; central disease;
KW regulated on activation, normal T cell expressed and secreted; allergy;
KW affinity compound; expression vector; CHO cell; viral disease;
KW infectious disease; tumour; hyperlipidaemia; hypercholesterolaemia.
OS Homo sapiens.
PN J09176048-A.
PF 28-DEC-1995; 342130.
PR 28-DEC-1995; JP-342130.
PA (TAKE ) TAKEDA CHEM IND LTD.
DR WPI; 97-399449/37.
DR N-PSDB; T86154.
PT Preparation of human MIP-1-alpha/RANTES receptor protein - used in
PT the treatment of viral diseases, tumours, allergy, diabetes
PT osteoporosis etc.
PS Disclosure; Page 15-16; 19pp; Japanese.
CC This sequence represents human MIP-1 alpha/RANTES receptor (macrophage
CC inflammatory protein 1 alpha/regulated on activation, normal T cell
CC expressed and secreted). The human MIP-1 alpha/RANTES receptor protein
CC may be used in a method for the screening of human MIP-1 alpha/RANTES
CC receptor affinity compounds. The MIP-1 alpha/RANTES receptor coding
CC sequence may be included in an expression vector, preferably pCCR, and
CC used to transform a CHO cell for use in the same method. The receptor
CC protein can provide a preventive and treating agent for viral diseases,
CC infectious diseases, tumours, allergy, diabetes, central diseases,
CC hyperlipidaemia, hypercholesterolaemia, osteoporosis, digestive ulcers,
CC etc.
SQ Sequence 355 AA;
Query Match 66.4%; Score 1834; DB 24; Length 355;
Best Local Similarity 63.0%; Pred. No. 1.32e-146;
Matches 225; Conservative 67; Mismatches 61; Indels 4; Gaps 4;
Db 1 metp-nttedydttefygdgdatp-cqkvnerafagallpplslvfyvlgilvgnllvvlv 58
Qy 1 MTTSLDVTVEFTGTS-Y-YDDVGLCEKADTRALMAQFVPLYSLVFTVGLGNVVMYMI 58
Db 59 lvqykrknmtsiylnlaisdlflftlplfwidylkddwvfgdamckllsgfytygly 118
Qy 59 LIKVRRLRIMTNIYLLNLAISDLFLVLPFWIHVVRGHNWVFGHGMCKLLSGFYHTGLY 118
Db 119 seiffilltdrylaihvafalrartvtfgvitsiilwalaalampglyfsktqgef 178
Qy 119 SEIFFIILLTDRLYLAIHVAFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELF 178
Db 179 thtcsfhphesirewklfgalnlgvlplvlmicytgikillrrpnekkaskav 238

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Qy 179 EETLCSALYPEDTVYSWRHFHTLMTIFCLVPLLVMAICYTGIIKTLRCPSSKKYKAI 238
Db 239 rlifvimiiflftwpyntllisvfdqflfthceqsrhldlavqvtviaythccvnp 298
Qy 239 RLIFVIMAVFFIWTPTYNVAILLSYOSILFGNDCERSKHLDLVNLVTEVAYSHCCMNP 298
Db 299 viyafvgerfrkylrqlfhrvavhlvkwplfslvdrsvstspstgehelsagf 355
Qy 299 VIYAFVGERFRKYLHRHFHRLHMLGRIYIFLPSEKLERISSTSSVSPSTAPPELSIVF 355
RESULT 11
W29179 standard; Protein; 355 AA.
W29179;
19-DEC-1997 (first entry)
DE Rat CC chemokine receptor.
KW Rat; CC chemokine receptor; screen; binding; ligand.
OS Rattus rattus.
PN J09227599-A.
PD 02-SEP-1997.
PR 22-FEB-1996; 035192.
PA (TAKE ) TAKEDA CHEM IND LTD.
DR WPI; 97-486426/45.
DR N-PSDB; T86839.
PT CC chemokine receptor protein - useful to screen for novel binding
PT compounds
PS Claim 1; Page 20-21; 26pp; Japanese.
CC This sequence is a rat CC chemokine receptor. The receptor can be used
CC to screen for novel binding compounds and for preparation of antibodies
CC or antiserum.
SQ Sequence 355 AA;
Query Match 62.5%; Score 1726; DB 24; Length 355;
Best Local Similarity 57.6%; Pred. No. 4.07e-137;
Matches 205; Conservative 88; Mismatches 61; Indels 2; Gaps 2;
Db 1 meis-nitetyptttdygdgpcqktdvrafgagllpplysfvfiigvgnllvlvl 59
Qy 1 MTTSLDVTVEFTGTSYD-DVGLCEKADTRALMAQFVPLYSLVFTVGLGNVVMYMI 59
Db 60 mqhrqlqsmtsiylfnlavsdvlfplfwidylkddwvfgdamckllsgfytygly 119
Qy 60 IKYRRLRIMTNIYLLNLAISDLFLVLPFWIHVVRGHNWVFGHGMCKLLSGFYHTGLY 119
Db 120 eiffilltdrylaihvafalrartvtfgvitsiilwalaalampglyfsktqgef 179
Qy 120 EIFFIILLTDRLYLAIHVAFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELF 179
Db 180 htcsphfpdeslktwrfqalknllglilplllmicyagiirillrrpnekkaskav 239
Qy 180 EETLCSALYPEDTVYSWRHFHTLMTIFCLVPLLVMAICYTGIIKTLRCPSSKKYKAI 239
Db 240 lifaiftllflwtpyntlvsvafgdlvfnqceqskldlavqvtviaythccvnp 299
Qy 240 LIFVIMAVFFIWTPTYNVAILLSYOSILFGNDCERSKHLDLVNLVTEVAYSHCCMNP 299
Db 300 iyvfvgerfrkylrqlfhrvavhlvkwplfslvdrsvstspstgehelsagf 355
Qy 300 IYAFVGERFRKYLHRHFHRLHMLGRIYIFLPSEKLERISSTSSVSPSTAPPELSIVF 355
RESULT 12
W27125 standard; Protein; 352 AA.
W27125;
14-DEC-1997 (first entry)
DE Macaque chemokine receptor 88C.
KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis;
KW tumour; asthma; viral infection; AIDS; inflammation;
KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
KW G protein coupled receptor; ligand; modulator; antibody.
OS Macaca sp.

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PN W09722698-A2.
PD 26-JUN-1997.
PF 20-DEC-1996; U20759.
PR 07-JUN-1996; US-661393.
PR 20-DEC-1995; US-575967.
PA (ICOS-) ICOS CORP.
PI Gray PW, Raport CJ, Schweickart VL;
DR WPI; 97-341689/31.
DR N-PSDB; T85163.
PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used
PT to modulate leukocyte trafficking, e.g. for treatment of
PT inflammation, tumours, viral infections, autoimmune diseases, etc.
PS Claim 36; Page 57-58; 65pp; English.
CC This polypeptide sequence comprises macaque chemokine receptor 88C,
CC a G protein coupled receptor that is involved in leukocyte
CC trafficking. Its amino sequence was deduced from a 88C DNA
CC (T85163) isolated by PCR amplification. It shows 97% identity to
CC human 88C (W27123). 88C receptors and their polypeptide fragments
CC can be produced in transformed host cells. The receptors, peptides
CC comprising one or more of the extracellular or intracellular
CC domains, and anti-receptor antibodies can be used to modulate
CC receptor activities, particularly ligand and G protein binding, and
CC are potentially useful in the treatment of
CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
CC infection, AIDS, inflammatory conditions, pathological immune
CC response, abnormal haematopoietic processes etc. A hybridoma
CC that produces an antibody that specifically binds to macaque 88C is
CC claimed.
SQ Sequence 352 AA;

      Query Match          54.2%; Score 1497; DB 24; Length 352;
      Best Local Similarity 55.2%; Pred. No. 4.95e-117;
      Matches 185; Conservative 84; Mismatches 57; Indels 9; Gaps 9;

Db 20 cqkinvkqiaarlpplyslvfigfvgmnlvlllnckrksmtidyllnlaisdlif 79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 24 CEKADTRALMAQFVPLYSLVFTVGLGNVVMVILIKYRRLRIMNTIYLLNLAISDLF 83
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 80 lltvpfwahyaaq-wdfgntmcqlltglyfigfgffgffillltidrylavhavfalk 138
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 84 LVTLPFWIHVYRGHNWVFGHGCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALR 143

Db 139 artvtfgvvtvitwvavfaslpigiftrsqreglhvt-csshfysq-yqfwnfqt1 196
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 144 ARTVFGVITSIVTWGLAVLAALPEFIFETE-ELFEETLCSALYPEDTVYS-WRHFFHL 201

Db 197 kmvilglvpllvmycysgilktllrcnrckhravrliftimivylfwapynvill 256
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 202 RMTIFCLVPLLVMAICYGTGIKTLRCPS-KKKYKAIRLIFVIMAVFIFWTPYNVAIL 260

Db 257 lntfqef-fglncssnrlldqamqvteitgmthccinpliyafvgekfrnyllvffqkh 315
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 261 LSSYQSILFG-NDCCRSKHLDLVLMVTEVIAVSHCCMNPVIAFVGERPKYLRHFFHRH 319

Db 316 iakrfckccsifqgeaperassvytrstgeqelsv 350
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 320 LLMHLGRYIPFLPSEKLENTSSV-SPSTAEPPELSI 353

RESULT 13
ID W27123 standard; Protein: 352 AA.
AC W27123.
DE Human chemokine receptor 88C.
KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis;
KW tumour; asthma; viral infection; AIDS; inflammation;
KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
KW G protein coupled receptor; ligand; modulator; antibody; human.
OS Homo sapiens.
FH Key Location/Qualifiers
FT domain 1..32
FT /label= Extracellular_domain
FT domain 56..67

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FT domain /label= Intracellular_domain
FT 89..112
FT /label= Extracellular_domain
FT 125..145
FT /label= Intracellular_domain
FT 166..191
FT /label= Extracellular_domain
FT 213..235
FT /label= Intracellular_domain
FT 259..280
FT /label= Extracellular_domain
FT 301..352
FT /label= Intracellular_domain
PN W09722698-A2.
PD 26-JUN-1997.
PF 20-DEC-1996; U20759.
PR 07-JUN-1996; US-661393.
PR 20-DEC-1995; US-575967.
PA (ICOS-) ICOS CORP.
PI Gray PW, Raport CJ, Schweickart VL;
DR WPI; 97-341689/31.
DR N-PSDB; T85161.
PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used
PT to modulate leukocyte trafficking, e.g. for treatment of
PT inflammation, tumours, viral infections, autoimmune diseases, etc.
PS Claim 16; Page 47-48; 65pp; English.
CC This polypeptide sequence comprises novel human chemokine receptor
CC 88C, a G protein coupled receptor that is involved in leukocyte
CC trafficking. Its amino sequence was deduced from a cDNA clone
CC (T85161) isolated from a macrophage library. It shows 62% identity
CC to CCKR1. Chemokine receptor 88-2B (see W27124) has also been
CC identified. 88C and 88-2B receptors and their polypeptide fragments
CC can be produced in transformed host cells. The receptors, peptides
CC comprising one or more of the extracellular or intracellular
CC domains, and anti-receptor antibodies can be used to modulate
CC receptor activities, particularly ligand and G protein binding, and
CC are potentially useful in the treatment of
CC atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
CC infection, AIDS, inflammatory conditions, pathological immune
CC response, abnormal haematopoietic processes etc.
SQ Sequence 352 AA;

      Query Match          53.8%; Score 1484; DB 24; Length 352;
      Best Local Similarity 54.3%; Pred. No. 6.81e-116;
      Matches 182; Conservative 87; Mismatches 57; Indels 9; Gaps 9;

Db 20 cqkinvkqiaarlpplyslvfigfvgmnlvlllnckrksmtidyllnlaisdlif 79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 24 CEKADTRALMAQFVPLYSLVFTVGLGNVVMVILIKYRRLRIMNTIYLLNLAISDLF 83

Db 80 lltvpfwahyaaq-wdfgntmcqlltglyfigfgffgffillltidrylavhavfalk 138
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 84 LVTLPFWIHVYRGHNWVFGHGCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALR 143

Db 139 artvtfgvvtvitwvavfaslpigiftrsqreglhvt-csshfysq-yqfwnfqt1 196
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 144 ARTVFGVITSIVTWGLAVLAALPEFIFETE-ELFEETLCSALYPEDTVYS-WRHFFHL 201

Db 197 kmvilglvpllvmycysgilktllrcnrckhravrliftimivylfwapynvill 256
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Qy 202 RMTIFCLVPLLVMAICYGTGIKTLRCPS-KKKYKAIRLIFVIMAVFIFWTPYNVAIL 260

Db 257 lntfqef-fglncssnrlldqamqvteitgmthccinpliyafvgekfrnyllvffqkh 315
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Qy 261 LSSYQSILFG-NDCCRSKHLDLVLMVTEVIAVSHCCMNPVIAFVGERPKYLRHFFHRH 319

Db 316 iakrfckccsifqgeaperassvytrstgeqelsv 350
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Qy 320 LLMHLGRYIPFLPSEKLENTSSV-SPSTAEPPELSI 353

RESULT 14
ID W27407 standard; Protein: 352 AA.

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Qy 202 RMTIFCLVPLLVMAICYTGIIKTLRCPS-KKKYKAIRLIFVIMAVFFIEWTPYNVAIL 260
Db 257 lntfqef-fglonccssnrlqamqvtetlqnmthccinpiliyafvgekfrnyllvffqkh 315
Qy 261 LSSYQSILFG-NDCERSKHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKYLRRHFHRH 319
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Qy 320 LLMLGRYIPFLPSEKLERTSSV-SPSTAPELSI 353

Search completed: Tue Dec 8 13:20:55 1998
Job time : 82 secs.

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WIRE

(TM)

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ch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 8 23:22:31 1998; MasPar time 1720.66 Seconds
Tabular output not generated. 1527.980 Million cell updates/sec

Title: >US-08-963-656-3
Description: (1-1193) from US08963656.seq
Perfect Score: 1193
N.A. Sequence: 1 TTGTCGTTATCCGGCAGCA.....TTGCCTTAAGAGGAGGACC 1193
Comp: AACACGAATAGCCCGTCT.....AACGGATTCTCCTTCCTGG

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 567134 seqs, 1101898692 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb155
1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in
7:em_om 8:em_or 9:em_ov 10:em_pat 11:em_ph 12:em_pl
13:em_ro 14:em_vl
genbank107
Database:
15:gb_bal 16:gb_ba2 17:gb_htg 18:gb_in 19:gb_om 20:gb_ov
21:gb_pat 22:gb_ph 23:gb_pl 24:gb_pl2 25:gb_pr1
26:gb_pr2 27:gb_pr3 28:gb_ro 29:gb_st 30:gb_sts 31:gb_sy
32:gb_un 33:gb_vl

Statistics: Mean 11.128; Variance 4.968; scale 2.240

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1112	93.2	1689	25	HSU49727 Human C-C chemokine re	0.00e+00
2	1110	93.0	1201	27	HSU28694 Human eosinophil CC ch	0.00e+00
3	1110	93.0	1717	25	HSU51241 Human eosinophil eotax	0.00e+00
4	1068	89.5	1068	26	AF026535 Homo sapiens chemokine	0.00e+00
5	962	80.6	1068	26	CAY13775 Cercopithecus aethiops	0.00e+00
6	956	80.1	1068	26	MMU13776 Macaca mulatta CCR-3	0.00e+00
7	952	79.8	1068	26	AF017283 Macaca mulatta chemoki	0.00e+00
8	576	48.3	1440	28	MMU28406 Mus musculus macrophag	0.00e+00
9	572	47.9	1185	28	MMU29677 Mus musculus chemokine	0.00e+00
10	562	47.1	1315	28	RNRPKR3 Rattus norvegicus mRNA	0.00e+00
11	555	46.5	1080	28	AF003954 Rattus norvegicus chem	0.00e+00
12	428	35.9	1495	25	HUMCCCKR1A Human C-C chemokine re	0.00e+00
13	428	35.9	1609	21	E13385 cDNA encoding human MI	0.00e+00

14	428	35.9	2156	21	I58541	Sequence 1 from patent	0.00e+00
15	428	35.9	2156	25	HUMRANTES	Homo sapiens macrophag	0.00e+00
16	428	35.9	2214	26	HUMHMI45	Human mRNA for HMI45.	0.00e+00
17	385	32.3	1068	26	AF017282	Macaca mulatta chemoki	0.00e+00
18	359	30.1	1544	21	E13732	cDNA encoding rat CC c	4.87e-298
19	351	29.4	1748	28	MMU28404	Mus musculus macrophag	1.72e-290
20	349	29.3	1068	28	MMU29678	Mus musculus chemokine	1.32e-288
21	276	23.1	1371	28	MMU28405	Mus musculus macrophag	4.94e-220
22	268	22.5	1844	27	EHVU20824	Equine herpesvirus 2,	1.48e-212
23	234	19.6	1457	28	RNCKR5	R.norvegicus mRNA for	6.84e-181
24	234	19.6	1689	28	RNU77350	Rattus norvegicus chem	6.84e-181
25	228	19.1	1078	28	AF022990	Mus musculus CC chemok	2.52e-175
26	228	19.1	2888	28	D83648	House mouse; Musculus	2.52e-175
27	227	19.0	1059	26	AF005661	Macaca nemestrina CC c	2.13e-174
28	227	19.0	1059	27	MMU96762	Macaca mulatta chemoki	2.13e-174
29	226	18.9	1060	26	AF011530	Homo sapiens isolate U	1.80e-173
30	225	18.9	1060	26	AF011538	Pan troglodytes isolat	1.52e-172
31	226	18.9	1125	28	MMU47036	Mus musculus MIP-1 alp	1.80e-173
32	223	18.7	1059	26	AF005658	Papio hamadryas CC che	1.09e-170
33	223	18.7	1059	26	AF005662	Macaca mulatta CC chem	1.09e-170
34	223	18.7	1059	27	MMU73739	Macaca mulatta CC chem	1.09e-170
35	223	18.7	1059	26	AF023452	Papio hamadryas anubis	1.09e-170
36	223	18.7	1059	26	AF005660	Macaca fascicularis CC	1.09e-170
37	223	18.7	1078	28	MMU83327	Mus musculus CC chemok	1.09e-170
38	223	18.7	1086	27	CAU83324	Cercopithecus aethiops	1.09e-170
39	223	18.7	1966	27	MMU77672	Macaca mulatta CC chem	1.09e-170
40	222	18.6	1059	26	AF005663	Pan troglodytes CC che	9.16e-170
41	222	18.6	1059	26	AF005659	Gorilla gorilla CC che	9.16e-170
42	222	18.6	1060	26	AF011513	Homo sapiens isolate M	9.16e-170
43	222	18.6	1060	26	AF011519	Homo sapiens isolate T	9.16e-170
44	222	18.6	1060	26	AF011509	Homo sapiens isolate K	9.16e-170
45	222	18.6	1060	26	AF011526	Homo sapiens isolate U	9.16e-170

ALIGNMENTS

RESULT 1	HSU49727	1689 bp	DNA	PRI	04-OCT-1996
LOCUS	Human C-C chemokine receptor 3 (CKR-3)	gene, complete cds.			
DEFINITION	Human C-C chemokine receptor 3 (CKR-3)	gene, complete cds.			
ACCESSION	U49727				
NID	91477560				
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1689)				
AUTHORS	Ponath,P.D., Qin,S., Post,T.W., Wang,J., Wu,L., Gerard,N.P., Newman,W., Gerard,C. and Mackay,C.R.				
TITLE	Molecular cloning and characterization of a human eotaxin receptor expressed selectively on eosinophils				
JOURNAL	J. Exp. Med. 183 (6), 2437-2448 (1996)				
MEDLINE	96281895				
REFERENCE	2 (bases 1 to 1689)				
AUTHORS	Ponath,P.D.				
TITLE	Direct Submission				
JOURNAL	Submitted (21-FEB-1996) Paul D. Ponath, Molecular Biology, LeukoSite, Inc., 215 First St., Cambridge, MA 02118, USA				
FEATURES	Location/Qualifiers				
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	/product="C-C chemokine receptor 3"				
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	/translation="MTTSLDVFETGTSYDDVGLLCEKADTRALMAQFVPPYSLV FTVGLLGNVVVVMILIKYRIRIMTNIYLLNLAISDLFLVLPFWIHYRGNWVFG				

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BASE COUNT 430 a 416 c 345 g 497 t 1 others
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Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 1114; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 227 ACTATGATGACGTGGCCCTGCTCTGTGAAAAGCTGTATACAGAGCACTGTATGGCCCACT 286
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Qy 138 ACTATGATGACGTGGCCCTGCTCTGTGAAAAGCTGTATACAGAGCACTGTATGGCCCACT 197
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Db 287 TTGTGCCCCCGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 346
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Qy 198 TTGTGCCCCCGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 257
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Db 407 TGGCCATTTCGACCTGCTCTTCCTGCTGACCCCTCCCAATTTGATCCACATGTCAGGG 466
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Qy 318 TGGCCATTTCGACCTGCTCTTCCTGCTGACCCCTCCCAATTTGATCCACATGTCAGGG 377
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Qy 378 GGCATACTGGGTTTTGGCCATGCACTGTGTAAGCTCCTCTCAGGGTTTTATCACACAG 437
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Qy 438 GCTGTACAGGAGATCTTTTTCATAAATCCTGCTGACAACTGACAGGTACCTGSCCATG 497
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Qy 498 TCCATGCTGTGTTGCCCTTCGAGCCCGGACTGTGCATTTTGGTGTGCTATCACCAGCATCG 557
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Qy 678 GGCATTTCCACACTCTGAGAAATGACCATCTTCTGCTGCTCTCCCTGCTGCTGCTGCTGCTG 737
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Qy 1158 AGGTAGATGCAAGAAATTCCTTAAGAGGAGGAGGACC 1193
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RESULT 2
LOCUS HSU28694 1201 bp mRNA PRI 16-MAY-1996
DEFINITION Human eosinophil CC chemokine receptor 3 mRNA, complete cds.
ACCESSION U28694
NID g1199579
KEYWORDS
SOURCE human.
ORGANISM

Homo sapiens
Eukaryota; Eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Combiere, C., Ahuja, S.K. and Murphy, P.M.
TITLE Cloning and functional expression of a human eosinophil CC
chemokine receptor

J. Biol. Chem. 270 (28), 16491-16494 (1995)
95348056
REFERENCE 2 (bases 1 to 1201)
AUTHORS Combiere, C., Ahuja, S.K. and Murphy, P.M.
TITLE Cloning and functional expression of a human eosinophil CC
chemokine receptor

J. Biol. Chem. 271 (18), 11034 (1996)
96210048
REFERENCE 3 (bases 1 to 1201)
AUTHORS Combiere, C.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-1995) Christophe Combadiere, NIAID, National
Institutes of Health, Building 10, Room 11N11, Bethesda, MD 20892,
USA

COMMENT On Feb 22, 1996 this sequence version replaced gi:881569.
[Erratum J. Biol. Chem. 270 (1995) 30235].
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AVLAALPEFIEYEREELEFELCSALYXEDTVSWRHFILRMTIFCLVPLPLVMAIC
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BASE COUNT 278 a 320 c 267 g 336 t
ORIGIN

Query Match 93.0%; Score 1110; DB 27; Length 1201;
Best Local Similarity 99.9%; Pred. No. 0.00e+00;
Matches 1116; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 18 CAGGAGAGTGAATGACAACTCAGTATAGATACAGTTGAGACCTTTGGTACCACATCCT 77
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Qy	498	TCCATGCTGTGTTTGCCCTTCGAGCCCGGACTGTCACTTTTGGTGTGTCATCAGCAGCATCG	557
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Qy	558	TCACCTGGGGGCTGGCAGTGTACGAGCTCTCTCGTAATTTATCTTCTATCAGACTGAAG	617
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Qy	618	AGTTGTTTGAAGAGACTCTTTTGCAAGTGTCTTTTACCAGAGAGATACAGTATATAGCTGGA	677
Db	791	GGCAATTTCCACACTCTGAGAAATGACCATCTTCTGTCTCGTTCTCCCTCTGCTCGTATGG	850
Qy	678	GGCAATTTCCACACTCTGAGAAATGACCATCTTCTGTCTCGTTCTCCCTCTGCTCGTATGG	737
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DEFINITION	Homo sapiens chemokine receptor (CCR3) mRNA, complete cds.		
ACCESSION	AF026535		
NID	92582565		
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
REFERENCE	Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS	1 (bases 1 to 1068)		
TITLE	Xiao, L., Weiss, S., Qari, S., Rudolph, D., Hodge, T. and Lal, R.		
JOURNAL	Partial resistance to infection by syncytium-inducing primary HIV-1		
REFERENCE	in exposed uninfected individuals homozygous for CCR5 32bp deletion		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 1068)		
JOURNAL	Qari, S.		
REFERENCE	Direct Submission		
TITLE	Submitted (24-SEP-1997) Retrovirus Diseases Branch, Centers for		
JOURNAL	Disease Control and Prevention, 1600 Clifton Road, Atlanta, GA		

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QY 752 GGAATCATCAAAACGCTGCTGAGGTGCCCGCCAGTAAAAAAGATACAGGCCATCCGGCTC 811
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QY 812 ATTTTGTGATCATGCGGGTGTTCATATTTCTGGACACCCCTACAAATGTGGCTATCCCTT 871
Db 781 CTCTCTTCCTATCAATCCATCTTATTGGAATGACTGTGAGGGAGCAGCATCTGGAC 840
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Db 841 CTGGTCTGCTGTGACAGAGGTGATCGCTACTCCCACTGCTGCTGATGAACCGGTGATC 900
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Db 901 TAGCCCTTTGTTGGAGAGAGTTCCGGAAGTACTCTGCGCACTTCTTCACAGGCACCTTG 960
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QY 1112 TCTGTCTCTCCATCCACAGAGCGGGAAGTCTCTATTGTGTTTAG 1159
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LOCUS CAY13775 1068 bp DNA PRI 16-FEB-1998
DEFINITION Cercopithecus aethiops CCR-3 gene.
ACCESSION Y13775
NID 92266433
KEYWORDS C-C chemokine receptor-3; CCR-3 gene.
SOURCE African green monkey.
ORGANISM Cercopithecus aethiops
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
Cercopithecus.
REFERENCE 1 (bases 1 to 1068)
AUTHORS Sol.N., Treboute.C., Gomas.E., Ferchal.F., Shacklett.B. and Alizon.M.
TITLE The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor for HIV-2, but not for HIV-1
JOURNAL Virology 240 (2), 213-220 (1998)
EDLINE 98118446
REFERENCE 2 (bases 1 to 1068)
AUTHORS Alizon.M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1997) M. Alizon, Institut Cochin de Genetique Moleculaire, ICGM, 22 rue Mechain, 75014 Paris, FRANCE
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Db 1021 TCTGTCTCTCTCCACAGAGCGGGAACCTCTGTATTGTGTTTAG 1068

Qy 1112 TCTGTCTCTCCATCCACAGAGAGCCGGAAGTCTCTATGTGTTTAG 1159

RESULT 6
LOCUS MMV13776 1068 bp DNA PRI 16-FEB-1998
DEFINITION Macaca mulatta CCR-3 gene.
ACCESSION Y13776
NID 92266685
KEYWORDS C-C chemokine receptor-3; CCR-3 gene.
SOURCE rhesus monkey.
ORGANISM Macaca mulatta
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
1 (bases 1 to 1068)
SOL, N., Treboute, C., Gomas, E., Ferchal, F., Shacklett, B. and
Alizon, M.
TITLE The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor
for HIV-2, but not for HIV-1
JOURNAL Virology 240 (2), 213-220 (1998)
MEDLINE 98118446
REFERENCE 2 (bases 1 to 1068)
AUTHORS Alizon, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1997) M. Alizon, Institut Cochin de Genetique
Moleculaire, ICM, 22 rue Mechain, 75014 Paris, FRANCE
FEATURES
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BASE COUNT 225 a 289 c 249 g 305 t
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1st Local Similarity 94.8%; Pred. No. 0.00e+00;
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LOCUS AF017283 1068 bp DNA PRI 18-SEP-1997
DEFINITION Macaca mulatta chemokine receptor (CCR3) gene, complete cds.
ACCESSION AF017283
NID 92407218
KEYWORDS rhesus monkey.
SOURCE Macaca mulatta
ORGANISM
REFERENCE 1 (bases 1 to 1068)
AUTHORS Hauer, D.A., Margulies, B.J. and Clements, J.E.
TITLE Direct Submission
JOURNAL Submitted (05-AUG-1997) Division of Comparative Medicine, Johns
Hopkins University School of Medicine, 720 Rutland Ave., Traylor
G-60, Baltimore, MD 21205, USA
FEATURES
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BASE COUNT 229 a 289 c 245 g 305 t
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LOCUS MMU28406 1440 bp DNA ROD 27-FEB-1996
DEFINITION Mus musculus macrophage inflammatory protein-1 alpha receptor-like
2 gene, complete cds.
ACCESSION U28406
NID g1203800
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 1440)
Gao, J. L. and Murphy, P. M.
Cloning and differential tissue-specific expression of three mouse
beta chemokine receptor-like genes, including the gene for a
functional macrophage inflammatory protein-1 alpha receptor
J. Biol. Chem. 270 (29), 17494-17501 (1995)
JOURNAL MEDLINE 95340546
REFERENCE 2 (bases 1 to 1440)
Gao, J. L.
Direct Submission
Submitted (05-JUN-1995) Ji-Liang Gao, Lab of Host Defenses, NIAID,
National Institutes of Health, Building 10, Room 11N113, Bethesda,
MD 20892, USA
COMMENT On Feb 27, 1996 this sequence version replaced gi:1199860.
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BASE COUNT 365 a 325 c 295 g 455 t
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QY 1013 TTCGGAAACACCTTGGGCTCTTTTCCACAGAAATGTGACGTTTACCTGGGAAATAT 1072
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Db 1220 ATTCATTTCTCTGTTGAGAAATGGAAGAACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1279
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QY 1073 ATTCATTTCTCTGTTGAGAAATGGAAGAACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1132
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[illegible]

RESULT	12	
LOCUS	HUMCCKR1A	1495 bp mRNA PRI 31-DEC-1994
DEFINITION	Human C-C chemokine receptor type 1 (C-C CKR-1) mRNA, complete cds.	
ACCESSION	L09230	
NID	g179984	
KEYWORDS	C-C chemokine receptor type 1.	
SOURCE	Homo sapiens	cDNA to mRNA.
ORGANISM	Homo sapiens	
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 1495)	
AUTHORS	Neote,K., DiGregorio,D., Mak,J.Y., Horuk,R. and Schall,T.J.	
TITLE	Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor	
JOURNAL	Cell 72 (3), 415-425 (1993)	
MEDLINE	93161416	
FEATURES	Location/Qualifiers	

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348 a 389 c 397 t

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Query Match      35.9%;   Score 428;   DB 25;   Length 1495;
Best Local Similarity 72.2%;   Pred. No. 0.00e+00;
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Db      219  CTTGAACCTGCCATTTCTTGACCTGCTCTTCTGTGTACAGCTTCCTCTCTGAGTCGACTA 278
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Qy      310  GCTCAACCTGCCATTTTCGGACCTGCTCTTCTCTGTCAACCCTCCATCTCTGGATCCACTA 369

Db      279  CAAGTTGAAGCATGACTGGGTTTTTGGTGTAGCCCATGTGAAGATCCCTCTCTGGGTTTTTA 338
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Qy      370  TGTcAGGGGCAATAcTGGGTTTTTGGCCATGGCAATGTGAAGCTCCCTCAGGGTTTTTA 429

Db      339  TTACACAGGCTTGACACGAGATCTTTTTTCATCATCTCGCTGACGATTGACAGGTACT 398
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Qy      430  TCACACAGGCTTGACACGAGATCTTTTTTCATATCTCTGCTGACAATCGACAGGTACT 489

Db      399  GGCCATCGTCCACGCCCGTGTGTGGCTTTCGGGCGACGGACCGCTCACTTTTGGTGCATCAC 458
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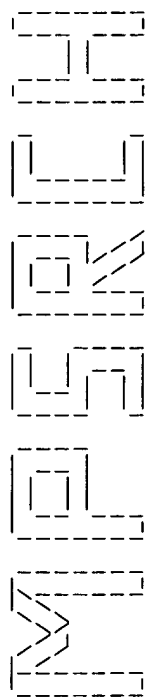
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Qy	670	TAGCTGGAGGCATTTCCACACTCTCGAATGACCATCTTCTGTCTCGTTCTCCCTCTGCT	729
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Qy	910	TGACGGGAGCAAGCATCTGGACCTGGTCATGCTGTGTACAGAGGTGATCGCTACTCCCA	969
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Qy	1150	TGTGTT	1155

RESULT	13	E13385	1609 bp	DNA	PAT	27-APR-1998
LOCUS		cDNA encoding human MIP-1 alpha /RANTES receptor.				
DEFINITION		E13385				
ACCESSION		G3252190				
NID		JP 1997176048-A/1.				
KEYWORDS		Homo sapiens.				
SOURCE		Homo sapiens				
ORGANISM		Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;				
REFERENCE		1 (bases 1 to 1609)				
AUTHORS		Honda,S. and Fujisawa,T. .				
TITLE		PRODUCTION OF HUMAN MIP-1ALPHA/PANTES RECEPTOR PROTEIN AND USE				
JOURNAL		Patent: JP 1997176048-A 1 08-JUL-1997;				
COMMENT		TAKEEDA CHEM IND LTD				
		OS Homo sapiens (human)				
		PN JP 1997176048-A/1				
		PD 08-JUL-1997				
		PF 28-DEC-1995 JP 1995342130				
		PI HONDA SUSUMU, FUJISAWA TOMOYUKI				
		PC A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00,A61K45/00				
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		PC C07K14/705,				

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QY	670	TAGCTGAGGCAATTTCCACACTCTGAGATGACCATCTCTGCTCTGCTCTCCCTGCT	729
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DEFINITION		Homo sapiens macrophage inflammatory protein-1-alpha/RANTES	
ACCESSION		L10918	
NID		9292416	
KEYWORDS		G-protein activator; G-protein coupled receptor; RANTES receptor; macrophage inflammatory protein-1-alpha.	
SOURCE		Homo sapiens (library: 2 kb HL-60 neutrophil cDNA in lambda-ZAP) cDNA to mRNA.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS		Gao J.-L., Tiffany, H.L., Kuhns, D., McDermott, D., Li, X., Francke, U.	
TITLE		Structure and functional expression of the human macrophage inflammatory 1 alpha (MIP-1alpha)/RANTES receptor	
JOURNAL		J. Exp. Med. 177, 1421-1427 (1993)	
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QY	310	GCTCAACCTGGCCATTTCTGGACCTGCTCTCTCTGCTGACCTTCCATTTCTGGATCCACTA	369
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Db	761	GAAATCCAAAGCTGTCGGTTGATTTTCTCATCATGATCATCTTTTCTCTCTTTGGAC	820
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(TM)

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ch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Wed Dec 9 01:11:26 1998; MasPar time 171.85 Seconds
Tubular output not generated. 944.517 Million cell updates/sec

Title: >US-08-963-656-3
Description: (1-1193) from US08963656.seq
Perfect Score: 1193
N.A. Sequence: 1 TTGTGCTTATCCGGGCAAGA.....TTGCTTAAGAGGAGGACC 1193
Comp: AACACGAATAGCCCGTTCT.....AACGGATTTCCTTCCTCGG

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 188442 seqs, 68026449 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 9.178; Variance 5.134; scale 1.788

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	ID	Description	Pred. No.
1	1193	100.0		T31335	CC-chemokine receptor	0.00e+00
2	1112	93.2		T31336	CC-chemokine receptor	0.00e+00
3	1112	93.2		T58783	Human C-C chemokine r	0.00e+00
4	1112	93.2		T31334	CC-chemokine receptor	0.00e+00
5	1110	93.0		T85162	Human chemokine recep	0.00e+00
6	1110	93.0		T93601	Human eosinophil eota	0.00e+00
7	1034	86.7		T79096	Human CCR3 chemokine	0.00e+00
8	428	35.9		T86154	Human MIP-1alpha/RAN	1.28e-295
9	428	35.9		T86295	C-C chemokine recepto	1.28e-295
10	428	35.9		T90384	Human MIP-1 alpha/RAN	1.28e-295
11	359	30.1		T86839	CDNA encoding rat CC	3.21e-243
12	223	18.7		T85163	Macaque chemokine rec	8.30e-141
13	220	18.4		T76920	DNA encoding human CC	1.44e-138

14	220	18.4	1255	39	T76919	DNA encoding human CC	1.44e-138
15	220	18.4	1414	25	T44042	Human G-protein chemo	1.44e-138
16	220	18.4	1477	37	T90117	CDNA for human CCR5.	1.44e-138
17	220	18.4	3383	34	T85161	Human chemokine recep	3.71e-105
18	175	14.7	1083	35	T96976	Human monocyte chemoa	3.71e-105
19	175	14.7	1979	15	O96298	Human monocyte chemoa	9.90e-101
20	169	14.2	2332	15	O96297	Human monocyte chemoa	3.07e-88
21	152	12.7	792	37	T90116	CDNA for inactive hum	3.07e-88
22	152	12.7	1442	37	T90118	CDNA for inactive hum	3.07e-88
23	152	12.7	1557	39	T99542	Human chemokine recep	3.07e-88
24	123	10.3	1607	23	T35277	Chemokine receptor K5	3.92e-67
25	76	6.4	1586	26	T44099	Human G-protein recep	7.65e-34
26	69	5.8	1900	11	O66162	Partial coding sequen	4.76e-29
27	69	5.8	2058	11	O66153	Putative seven trans	4.76e-29
28	69	5.8	2154	11	O64125	Epstein Barr virus in	4.76e-29
29	69	5.8	2160	11	O66160	Putative seven trans	4.76e-29
30	65	5.4	2751	11	O66164	Seven transmembrane r	2.44e-26
31	60	5.0	1162	11	O66170	Seven transmembrane r	5.48e-23
32	60	5.0	2254	11	O66167	Seven transmembrane r	5.48e-23
33	55	4.6	1119	40	V15418	Human dendritic cell	1.11e-19
34	53	4.4	1373	17	O99951	Recombinant high affi	2.26e-18
35	51	4.3	1316	39	T99543	Human chemokine recep	4.49e-17
36	51	4.3	1547	40	V15419	Human macrophage/dend	4.49e-17
37	49	4.1	1200	5	O30011	Sequence encoding a h	8.72e-16
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39	48	4.0	1176	17	O99950	Recombinant high affi	3.81e-15
40	48	4.0	1883	17	O99906	Interleukin 8 recepto	3.81e-15
41	48	4.0	1933	5	O29505	Interleukin-8 recepto	3.81e-15
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43	44	3.7	514	23	T35278	Chemokine receptor CD	1.30e-12
44	43	3.6	1373	5	O30013	Sequence encoding a l	5.47e-12
45	43	3.6	1748	17	O99908	Interleukin 8 recepto	5.47e-12

ALIGNMENTS

RESULT 1
ID T31335 standard; cDNA; 1193 BP.
AC T31335;
DT 15-NOV-1996 (first entry)
DE CC-chemokine receptor 3 cDNA clone.
KW CC-chemokine receptor 3; CKP-3; Bos-L2; inhibitor; antisense;
KW antiinflammatory; eosinophil; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 92..1159 /*tag= a
FT variation 918..919 /*tag= b
FT FT /note= "CKR-3 cDNA clone has GC at positions
FT 918-919, coding for serine (AGC) at
FT position 276; a genomic clone has CG at
FT these positions, coding for threonine
FT (AGC)"
PN W09622371-A2.
PD 25-JUL-1996.
PE 19-JAN-1996; U00608.
PR 19-JAN-1995; US-375199.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (LEUK-) LEUKOSITE INC.
PA Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
Qin S;
DR WPI: 96-354528/35.
DR P-PSDB: W03377.
PT Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
PS Claim 1; Page 111-113; 153pp; English.
CC A genomic DNA clone (T31335) codes for a novel receptor (W03377),
CC designated Eos L2 or C-C chemokine receptor 3 (CKR-3), involved
CC in leukocyte migration associated with inflammation. It was
CC isolated from a human library constructed from eosinophils obtd.

CC from a patient with hyper-eosinophilic syndrome using a probe
CC (P4 cDNA) encoding the MIP-1alpha/RANTES receptor. A CCR-3
CC genomic clone (T31334) was also isolated, and a consensus sequence
CC is given in T31336. The cDNA and genomic clones can be used for
CC the prodn. of recombinant CCR-3 in host cells, or to design
CC antisense sequences useful for treating inflammatory disease.
SQ Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T;

Query Match 100.0%; Score 1193; DB 23; Length 1193;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 TACTTAGAAGAGATTTTCAGGGAGAGTGAATGACACACCTCACTAGATACAGTTGAGAC 120
Db 121 ctttggtaccacactactatgatgacgtgggacctgtctgtgaaagaagtgtataccag 180
Qy 121 CTTTGGTACCACATCCTACTATGATGACGTGGCGCTGCTCTGTGAAAGAGCTGATACCAG 180
Db 181 agcactgatgcccagtttgtcccccgctgtactccctgtgttcaactgtgggaccttt 240
Qy 181 AGCACTGATGCCCCAGTTGTGCCCCCGCTGTACTCCCTGGGTTCACGTGGGCGCTTT 240
Db 241 gggcaatgtgggtgggtgatgacctcataaaatcacaggagggtccgaattatgaccaa 300
Qy 241 GGGCAATGTGGTGGTGATGCTCTATTAATACAGGAGGCTCCGAATATGACCA 300
Db 301 catctacatgctcaacctggccatttcggacctgtctctcctgtcaaccttccatttg 360
Qy 301 CATCTACCTGCTCAACCTGGCCATTTCCGAGCTGCTCTTCCTCGTCAACCTTCCATTCTG 360
Db 361 gatccactatgtaggggacataactgggttttggccatggcagtgatgtaagctccctc 420
Qy 361 GATCCACTATGTCAGGGGGCAATACTGGGTTTTTGGCCATGGCATGTAGTCCCTCTC 420
Db 421 aggggttttatcacacagagctttgacagcagatctttttcataatcctgtgcacaatoga 480
Qy 421 AGGGTTTTATCACACAGAGCTTGTACAGCGAGATCTTTTTCATATCTCGTGACAAATCGA 480
Db 481 caggtaacctggccattgtccatgtgtgttggcccttgacggccgagctgcaattttgg 540
Qy 481 CAGGTACCTGGCCATTGTCCATGTGTGTGTGGCCCTTCGAGCGGGAGCTGTCACTTTTGG 540
Db 541 tgtcatccagcactgcacactggggcctggcagtgtagcagctcttctgtaatttat 600
Qy 541 TGTTCATCACAGCATGTCACCTGGGGCTGGCAGTGGTGTAGCAGCTCTCTCTGAATTTAT 600
Db 601 cttctatgagactgaagagttgtttgagagagactctttgacgtgctctttaccagagga 660
Qy 601 CTTCTATGAGACTGAAGAGTGTGTTGAGAGACATCTTTGACGTGCTCTTTACCCAGAGGA 660
Db 661 tacagtatagctggaggcattttccacactctgagaatgacctcttctgtctcgttct 720
Qy 661 TACAGTATATAGCTGGAGGCATTTCCACACTCTGAGATGACCATCTTCTCTCGTTCT 720
Db 721 cccctctgctgttatggccatctgtctacacaggaatacataaaacgctgtgaggtgcc 780
Qy 721 CCCCTCTGCTGTTTGGCCATCTGCTACACAGGAATCATCAAAACGCTGTGAGGTGCC 780
Db 781 cagtaaaaaaagatacaggccatccgctcatctttttgcatcatggcggtgtttttcat 840
Qy 781 CAGTAAAAAAGATACAGGCCATCCGGCTCATTTTCTCATCATGGCGGTGTTTTCAT 840
Db 841 ttcttgacacccctacaatgtgggtatccttctctctcttccatccatcttatttg 900
Qy 841 TTTCTGGACACCTACAATGTGGGTATCCTTCTCTCTCTCTATCAATCCATCTTATTGG 900
Db 901 aaatgactgtgagcggagcaagcatctggacctgtgacaggtgtgacaggtgtgacgc 960

Qy 901 AAATGACTGTGAGCGGAGCAAGCATCTGGACCTGGTATGCTGTGATGAGAGGTGATCGC 960
Db 961 ctactccactgctgcatagaaccgggtgatcagcctttgttgagagaggttccggaa 1020
Qy 961 CTACTCCCACTGCTGCATGAACCGGTGATCTAGCCCTTTGTTGGAGAGAGTTCCGGAA 1020
Db 1021 gtactcgcacactttctccacaggcactgtctcatcgaactggcgagatataccatt 1080
Qy 1021 GTACTCGCCCACTTCTTCCACAGGCACCTTGCTCATGACCTGGCGAGATACATCCCAT 1080
Db 1081 cttctctagtagaagctgaaagaacacacactgtctctccatccacagcagagccgga 1140
Qy 1081 CCTTCTTAGTAGAAGCTGGAAGAACACAGCTCTGTCTCTCCATCCACAGCAGACGGGA 1140
Db 1141 actctctattgtgttttaggtagatgcagaaaattgcctaaaggaggagacc 1193
Qy 1141 ACTCTCTATTGTGTTTATGAGTAGATGCAGAAAATTGCTTAAGAGGAGGACC 1193

RESULT 2
ID T31336 standard; DNA; 1116 BP.
AC T31336;
DT 15-NOV-1996 (first entry)
DE CC-chemokine receptor 3 consensus DNA sequence.
KW CC-chemokine receptor 3; CCR-3; Eos-L2; inhibitor; antisense;
KW antiinflammatory; eosinophil; ds.
OS Homo sapiens.
PN W09622371-A2.
PD 25-JUL-1996.
PF 19-JAN-1996; U00608.
PR 19-JAN-1995; US-375199.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (LEUK-) LEUKOSTE INC.
PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
PI Qin SJ;
DR WFI; 96-354528/35.
DR P-PSDB; W03378.
PT Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
PS Claim 1; Page 114-115; 153pp; English.
CC A consensus DNA sequence (T31336) codes for a novel human receptor
CC (W03378), designated Eos L2 or C-C chemokine receptor 2 (CCR-3).
CC It was deduced by comparing a genomic clone (T31334) and a cDNA
CC clone (T31335) coding for CCR-3 proteins (W03376 and W03377) having
CC slightly different sequences. Initial sequence information revealed
CC 2 regions in which the cDNA sequence appeared to be shifted in
CC frame, resulting in 2 sets of 4 contiguous amino acid differences
CC in the predicted proteins. Further sequence analysis revealed only
CC a single difference between the 2 open reading frames, the genomic
CC clone coding for threonine at position 276 and the cDNA clone for
CC serine.
SQ Sequence 1116 BP; 246 A; 286 C; 257 G; 306 T;

Query Match 93.2%; Score 1112; DB 23; Length 1116;
Best Local Similarity 98.0%; Pred. No. 0.00e+00;
Matches 1094; Conservative 20; Mismatches 2; Indels 0; Gaps 0;

Db 1 caggagagaagtgaatgacaacctcactagatagacagttgagaccttgggtaccacacct 60
Qy 78 CAGGAGAAGTGAATGACAACCTCACTAGATACAGTTGAGACCTTTGGTACCACATCTCT 137
Db 61 actatgatgacgtggcgctactctgtgaaagactgtacacagcactatggtccagct 120
Qy 138 ACTATGATGACGTGGGCTGCTCTGTGAAAAGCTGTATACAGAGCACTGATGCCCAT 197
Db 121 ttgtgcccccgctgtactccctggtgttcaactgtggcctcttgggcaatgtggtg 180
Qy 198 TTGTGCCCCGCTGTACTCCTCGTGTCTACTGTGGGCCCTCTTGGGCAATGTGTGTGG 257
Db 181 tgatgatcctcataaaatacaggaggtcctcgaattatgacacacatacctgctcaacc 240

[illegible]

interstitial; ILD: idiopathic pulmonary fibrosis;
rheumatoid arthritis; systemic; lupus erythematosus; SLE;
ankylosing spondylitis; scleritis; Sjorgen's; polymyositis;
dermatomyositis; bowel; anaphylaxis; drug; penicillin;
cephalosporin; insect sting; Crohn's; ulcerative colitis;
spondyloarthropathy; scleroderma; psoriasis; dermatosis;
dermatitis; eczema; atopic; urticaria; necrotising; cutaneous;
vasculitis; myositis; fascitis; multiple sclerosis;
myasthenia gravis; juvenile onset diabetes; glomerulonephritis;
autoimmune; thyroiditis; Bechet's; graft; rejection;
transplantation; allograft; graft versus host; cancer;
leukocyte infiltration; reperfusion injury; atherosclerosis;
haematologic malignancy; septic; endotoxic; shock;
polymyositis; dermatomyositis; immunosuppression; immunodeficiency;
AIDS; radiation therapy; chemotherapy; autoimmune; corticosteroid;
C-C chemokine receptor 3; CRK3; ss.
Homo sapiens.

Key	Location/Qualifiers
cds	181..1248
	/*tag= a
	/product= CRK3

WO9700960-A1.
09-JAN-1997.
21-JUN-1996; U10723.
23-JUN-1995; US-494093.
(LEUK-) LEUKOSITE INC.
MacKay C, Newman W, Ponath PD, Qin S, Ringler DJ;
WPI: 97-087387/08.
P-PSDB: W10100.

New isolated human ectaxin gene - used to develop prods. for the diagnosis and treatment of e.g. inflammation, allergies, auto-immune disease, infections and tumours
Example 7; Page 97; 130pp; English.
The present sequence encodes human C-C chemokine receptor 3 (CRK3), to which human ectaxin (hE), an eosinophil specific chemoattractant capable of stimulating eosinophil accumulation and/or attracting eosinophils (including chemotaxis), binds.
hE can be used to develop products for the diagnosis, prevention or treatment of hE associated diseases or conditions. The products can be used to treat inflammatory or allergic diseases and conditions, including respiratory allergic diseases (e.g. asthma, allergic rhinitis, hypersensitivity lung diseases or pneumonitis, eosinophilic pneumonias such as Loeffler's syndrome and chronic eosinophilic pneumonia, interstitial lung diseases (ILD) such as idiopathic pulmonary fibrosis or ILD associated with rheumatoid arthritis, systemic lupus erythematosus (SLE), ankylosing spondylitis, systemic sclerosis, Sjorgen's syndrome, polymyositis or dermatomyositis), systemic anaphylaxis or hypersensitivity responses, drug allergies (e.g. to penicillin and cephalosporins), insect sting allergies, inflammatory bowel diseases (e.g. Crohn's disease and ulcerative colitis), spondyloarthropathies, scleroderma, psoriasis and inflammatory dermatoses (e.g. dermatitis, eczema, atopic dermatitis, allergic contact dermatitis, urticaria and necrotising, cutaneous and hypersensitivity vasculitis), eosinophilic myositis and fascitis, multiple sclerosis, SLE, myasthenia gravis, juvenile onset diabetes, glomerulonephritis, autoimmune thyroiditis, Bechet's disease, graft rejection (e.g. in transplantation) including allograft rejection or graft versus host disease and cancers with leukocyte infiltration of the skin or organs. The products can also be used to treat other diseases or conditions requiring the inhibition of undesirable inflammatory responses, including reperfusion injury, atherosclerosis, certain haematologic malignancies, cytokine induced toxicity (e.g. septic or endotoxic shock), polymyositis, dermatomyositis, immunosuppression (e.g. in individuals with immunodeficiency syndromes such as AIDS, undergoing radiation therapy, chemotherapy, therapy for autoimmune disease or other drug therapy, such as corticosteroid therapy, which causes immunosuppression), immunosuppression due to (e.g. congenital) deficiency (e.g. in ectaxin) or infectious diseases such as parasitic diseases.
Degenerate primers based on the guinea pig ectaxin amino acid sequence were used for the reverse transcriptase polymerase chain

CC reaction (RT-PCR) amplification of RNA isolated from inflamed,
CC eosinophilic lung tissue obtained from Balb/c mice sensitised to
CC ovalbumin. The amplification product was used as a probe to screen
CC a human genomic library in vector EMBL3 SP7/T7 to obtain the hE
CC gene.
SQ Sequence 1689 BP; 431 A; 416 C; 344 G; 497 T;

Query Match 93.2%; Score 1112; DB 32; Length 1689;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 1114; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 167 caggagagaagtgaatgacaacctcactagatcacagttgagacaccttggtagccacatcct 226
Qy 78 CAGGAGAGAGTGAATGACAACCTCAGTATGATGAGACCTTTGGTACCATCTCT 137

Db 227 actatgatgacgtgggctgctctgtaaaagctgataccagagcactgagccagct 286
Qy 138 ACTATGATGACGTGGCCCTGCTCTGTGAAAAAGCTGATACACAGACACTGATGGCCAGT 197

Db 287 ttgtgtcccccgctgtactccctgtgttcactgtgttgccctcttgggcaatgtgggtgg 346
Qy 198 TTGTGTCCCCCGCTGTACTCCCGTGGTGTTCACGTGTGGGCTCTTGGGCAATGTGGTGGTGG 257

Db 347 tgatgatctctataaaatcacagagcgctccgaattatgaccaacatctacctgctcaacc 406
Qy 258 TGATGATCTCTATAAATACAGAGAGCTCCGAATATGACCAACATCTACCTGCTCAACC 317

Db 407 tggccattcgagcctgtcttctcctcgtcacccttccattctggatccactatgtcgagg 466
Qy 318 TGGCCATTTCGACCTGCTCTTCCCTCGTCACCTTCCATTCGGATCCACATGATGTCAGGG 377

Db 467 ggcataactgggtttttggccatgcatgtgtaagctcctctcaggggtttttatcacag 526
Qy 378 GGCATAACTGGGTTTTTGGCCATGGCATGTGTAACTCTCTCAGGGTTTTATCATCACAG 437

Db 527 gctgtacagcgagatcttttcataactcctgctgacaatgacaggtacacctggccattg 586
Qy 438 GCTTGTACAGCAGATCTTTTCATTAATCCGTCGTCACAAATCGACAGGATACCTGGCCATG 497

Db 587 tccatgtgtgtttgcccctcgagcccgagctgtcacttttgggttcacaccagcagctcg 646
Qy 498 TCCATGCTGTGTTTGCCCTTCGAGCCGAGCTGTACATTTTGGTGTCTATCACCAGCATCG 557

Db 647 tcaactggggcctggcagctagcagctcttctcctgaatttatcttctatgagacgaag 706
Qy 558 TCACCTGGGGCTGGCAGTGTAGCAGCTCTTCCTGAAATTTATCTTCTATGAGACTGAAG 617

Db 707 agttgttgagagagactcttttcagctgctcttaccagagagatcacagtatatagctgga 766
Qy 618 AGTTGTTTGAAGAGACTCTTTCAGTGTCTTTTACCCAGAGGATACAGTATATAGCTGGA 677

Db 767 ggcatttcacactgtgagaatgacacattctgtgtctcgtttctcctctgctgtattgg 826
Qy 678 GGCATTTCACACTCTGAGAAATGACCATCTTCTGTCTCGTCTCCTCTCGCTGTATGG 737

Db 827 ccattgtctacacagaatcatcaaaagctgctgaggtgccccagtaaaaaaagtaca 886
Qy 738 CCATCTGTACACAGGAATCATCAAAAGCCTGTGAGTGGCCCGCCAGTAAAAAAGTACA 797

Db 887 agggccatccggctcattttgtcatcatggcggtgttttcatctttctggacaccctaca 946
Qy 798 AGGCCATCCGGCTCATTTTGTGTCATCATGGCGGTGTTTTTCATTTTCTGGACACCTTACA 857

Db 947 atgtggctatcctctctctctctcatcattccatttattggaaatgactgtgagcga 1006
Qy 858 ATGTGGCTATCTCTCTCTCTCTCAATCAATCATCTTATTGGAATGACTGTGAGCGGA 917

Db 1007 ggaagcatctggacctgctgctggtgtagacagaggtgatcgctactccccactgctga 1066
Qy 918 GCAAGCATCTGGACCTGGTGTATGTGGTGACAGAGAGGTGATCGCCTTACCTCCCACTGCTCA 977

Db 1067 tgaaccccggtgatccagcctttgtgtgagagaggttccggaagtaccttgcgacctct 1126
Qy 1126 TGAACCCCGGTGATCCAGCCTTTGTGTGAGAGAGGTTCGGAAGTACCTTGCGCCCTCT 1126

Qy 978 TGAACCCGGTGATCTACGCCCTTTGTGTGAGAGAGGTTCGGAGTACCTGCGCCACTTCT 1037
Db 1127 tccacagcactgtctcactgacatggcagatcacatccattctctctagttagaagc 1186
Qy 1038 TCCACAGCAGCTTGTCTATGCACCTGGCAGATACATCCCATTTCTTCTAGTGAAGC 1097

Db 1187 tggaaagaacacagctctgtctctccatccacagcagagccggaactctctattgtgttt 1246
Qy 1098 TGGAAAGAACACAGCTCTGTCTCTCATCCACAGAGAGCGGAACTCTCTATTGTGTTT 1157

Db 1247 aggtagatgcagaaattgcctaaagagagagacc 1282
Qy 1158 AGGTAGATGCAGAAAATTCCTTAAGAGAGAGGACC 1193

RESULT 4
ID T31334 standard; DNA; 1689 BP.
AC T31334;
DT 15-NOV-1996 (first entry)
DE CC-chemokine receptor 3 genomic DNA.
KW CC-chemokine receptor 3; CKP-3; Eos-L2; inhibitor; antisense;
KW antiinflammatory; eosinophil; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 181..1248
FT /*tag= a
FT variation 1007..1008
FT /*tag= b
FT /note= "CKR-3 genomic clone has CG at positions
FT 1007-1008, coding for threonine (ACG) at
FT position 276; a cDNA clone has GC at
FT these positions, coding for serine (AGC)"
FT misc_difference 1291
FT /*tag= c
FT /note= "base n at position 1291 is not identified
FT in the specification"
PN W09622371-A2.
PD 25-JUL-1996.
PF 19-JAN-1996; U00608.
PR 19-JAN-1995; US-375199.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (CHIL-) CHILDRENS MEDICAL CENT.
PA (LEUK-) LEUKOSITE INC.
PI Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
PI Qin S;
PI WPI; 96-354528/35.
DR P-PSDB; W03376.
DR Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
PS Claim 1; Page 109; 153pp; English.
CC A genomic DNA clone (T31334) codes for a novel receptor (W03376),
CC designated Eos L2 or C-C chemokine receptor 3 (CKR-3), involved
CC in leukocyte migration associated with inflammation. It was
CC isolated from a human genomic library in EMBL3 SP7/T7 vector by
CC screening with a PCR fragment generated from eosinophil cDNA
CC using degenerate primers (see also T31337-44). A CKR-3 cDNA
CC clone (T31335) was also isolated, and a consensus sequence is
CC given in T31336. The genomic and cDNA clones can be used for
CC the prodn. of recombinant CKR-3 in host cells, or to design
CC antisense sequences useful for treating inflammatory disease.
SQ Sequence 1689 BP; 431 A; 416 C; 344 G; 497 T;

Query Match 93.2%; Score 1112; DB 23; Length 1689;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 1114; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 167 caggagagaagtgaatgacaacctcactagatcacagttgagacaccttggtagccacatcct 226
Qy 78 CAGGAGAGAGTGAATGACAACCTCAGTATGATGAGACCTTTGGTACCATCTCT 137

Db 227 actatgatgacgtgggctgctctgtaaaagctgataccagagcactgagccagct 286
Qy 138 ACTATGATGACGTGGCCCTGCTCTGTGAAAAAGCTGATACACAGACACTGATGGCCAGT 197

Db 287 ttgtgtcccccgctgtactccctgtgttcactgtgttgccctcttgggcaatgtgggtgg 346
Qy 198 TTGTGTCCCCCGCTGTACTCCCGTGGTGTTCACGTGTGGGCTCTTGGGCAATGTGGTGGTGG 257

Db 347 tgatgatctctataaaatcacagagcgctccgaattatgaccaacatctacctgctcaacc 406
Qy 258 TGATGATCTCTATAAATACAGAGAGCTCCGAATATGACCAACATCTACCTGCTCAACC 317

Db 407 tggccattcgagcctgtcttctcctcgtcacccttccattctggatccactatgtcgagg 466
Qy 318 TGGCCATTTCGACCTGCTCTTCCCTCGTCACCTTCCATTCGGATCCACATGATGTCAGGG 377

Db 467 ggcataactgggtttttggccatgcatgtgtaagctcctctcaggggtttttatcacag 526
Qy 378 GGCATAACTGGGTTTTTGGCCATGGCATGTGTAACTCTCTCAGGGTTTTATCATCACAG 437

Db 527 gctgtacagcgagatcttttcataactcctgctgacaatgacaggtacacctggccattg 586
Qy 438 GCTTGTACAGCAGATCTTTTCATTAATCCGTCGTCACAAATCGACAGGATACCTGGCCATG 497

Db 587 tccatgtgtgtttgcccctcgagcccgagctgtcacttttgggttcacaccagcagctcg 646
Qy 498 TCCATGCTGTGTTTGCCCTTCGAGCCGAGCTGTACATTTTGGTGTCTATCACCAGCATCG 557

Db 647 tcaactggggcctggcagctagcagctcttctcctgaatttatcttctatgagacgaag 706
Qy 558 TCACCTGGGGCTGGCAGTGTAGCAGCTCTTCCTGAAATTTATCTTCTATGAGACTGAAG 617

Db 707 agttgttgagagagactcttttcagctgctcttaccagagagatcacagtatatagctgga 766
Qy 618 AGTTGTTTGAAGAGACTCTTTCAGTGTCTTTTACCCAGAGGATACAGTATATAGCTGGA 677

Db 767 ggcatttcacactgtgagaatgacacattctgtgtctcgtttctcctctgctgtattgg 826
Qy 678 GGCATTTCACACTCTGAGAAATGACCATCTTCTGTCTCGTCTCCTCTCGCTGTATGG 737

Db 827 ccattgtctacacagaatcatcaaaagctgctgaggtgccccagtaaaaaaagtaca 886
Qy 738 CCATCTGTACACAGGAATCATCAAAAGCCTGTGAGTGGCCCGCCAGTAAAAAAGTACA 797

Db 887 agggccatccggctcattttgtcatcatggcggtgttttcatctttctggacaccctaca 946
Qy 798 AGGCCATCCGGCTCATTTTGTGTCATCATGGCGGTGTTTTTCATTTTCTGGACACCTTACA 857

Db 947 atgtggctatcctctctctctctcatcattccatttattggaaatgactgtgagcga 1006
Qy 858 ATGTGGCTATCTCTCTCTCTCTCAATCAATCATCTTATTGGAATGACTGTGAGCGGA 917

Db 1007 ggaagcatctggacctgctgctggtgtagacagaggtgatcgctactccccactgctga 1066
Qy 918 GCAAGCATCTGGACCTGGTGTATGTGGTGACAGAGAGGTGATCGCCTTACCTCCCACTGCTCA 977

Db 1067 tgaaccccggtgatccagcctttgtgtgagagaggttccggaagtaccttgcgacctct 1126
Qy 1126 TGAACCCCGGTGATCCAGCCTTTGTGTGAGAGAGGTTCGGAAGTACCTTGCGCCCTCT 1126

QY 138 ACTATGATGACGTGGCCCTGCTCTGTGAAAAAGCTGATACACAGACACTGATGGCCCACT 197
Db 287 ttgtgccccgcctgtactccctggatttcaactgtgagccctcttggcaaatgtggtgag 346
QY 198 TTGTGCCCCGCGTGTACTCCCTGGTGTTCACCTGGGCCCTCTTGGCAATGTGGTGTG 257
Db 347 tgatgatcctcataaaataacagagagctccgaattatgaccaaactctacctgctcaacc 406
QY 258 TGATGATCCTCATAAAATACAGAGAGCTCCGAATTTATGACCAACATCTACCTGCTCAACC 317
Db 407 tggccatttcggaccctgtcttctctcgttcaaccctccattcttgatccactatgtcaggg 466
QY 318 TGGCCATTTTCGACCTGCTCTTCTCTGTCACCTTCCATTTCTGGATCCACTATGTGAGGG 377
Db 467 ggcataactgggtttttggccatggcatgtgtaagctctctcagggtttttatcacacag 526
QY 378 GGCATAACTGGGGTTTTTGGCCATGGCATGTGTAAAGCTCTCTCAGGGTTTTTATCACACAG 437
Db 527 gctgttacagcagagatctttttcataatcctcgtcgtgacaatcgacaggttacctggccattg 586
QY 438 GCTGTAGACGAGATCTTTTTCATATCTCTGCTGACATCGACAGGTACCTGGCCATTTG 497
Db 587 tccatcgtgtgttgccttcgagcccgagctgtcacttttgggtgtcaccacagcatcg 646
QY 498 TCCATGCTGTGTTTGGCCCTTCGAGCCCGGACTGCTCACTTTTGGTGTATCATCACCAGCATCG 557
Db 647 tcaactggggcctggcagtgctagcagctcttctcgaattattctctatgagactgaag 706
QY 558 TCACCTTGGGGCCTGGCAGTGTACAGAGCTCTTCTGAAATTTATCTCTATGAGACTGAAG 617
Db 707 agtgtttgaagagactctttcagtgctctttaccacagaggtacagatatagctgga 766
QY 618 AGTGTGTTGAAGAGACTCTTTGACGTGCTCTTTACCAGAGGATACAGTATAGCTGGA 677
Db 767 ggcatttcacacactctgagaatgacctctctgtctcgtcttccctcgtcgtcttatgg 826
QY 678 GGCATTTCCACACTCTGAGAAATGACCATCTCTGCTGCTTCTCCCTCTGCTGTTATGG 737
Db 827 ccaatctgtacacaggaatcataaaacgctgctgaggtgcccagtaaaaaaagtaca 886
QY 738 CCATCTGTACACAGGAATCATCAAAACGCTGCTGAGGTGCCCCAGTAAAAAAAGTACA 797
Db 887 aggcacatcgggctcattttgtcatcatggcggtgtttttcattttcttgacacccctaca 946
QY 798 AGCCCATCCGGCTCATTTTGTGTCATGCGCGGTGTTTTTCATTTTCTGGACACCCCTACA 857
Db 947 atgtggctatcctctctctctcctatcaatccatcttatttggaaatgactgtgagcgga 1006
QY 858 ATGTGGCTATCCTCTCTCTCTCTATCAATCCATCTATTGGAATGACTGTGAGCGGA 917
Db 1007 cgaagcatctggaccctgggtgctgctggtgacagaggtgatcgccactcctcactgtgca 1066
QY 918 GCAAGCATCTGGACCTGGTCTGCTGCTGACAGAGGTGATCGCCTACTCCCACTGCTGCA 977
Db 1067 tgaacccggtgatctacgcttcttggagagaggttccggaagtacacctgcgcacttct 1126
QY 978 TGAACCCGGTGATCTACGCTTTTGTGGAGAGAGGTTCGGGAAGTACCTCGCCACTTCT 1037
Db 1127 tccacagggcaacttgctcatgcaactcctgggagatacatcccatcctcctcctagtgagaagc 1186
QY 1038 TCCACAGGCACCTTGCTCATGCACTGGGACAGATACATCCCATTTCTTCTTAGTGAAGC 1097
Db 1187 tggaaagaacacagctctgtctctccatccacagcagagcgggaactctctattgtgttt 1246
QY 1098 TGGAAAGAACCACTGCTGTCTCTCCATCCACAGCAGAGCCGGAACCTCTCTATTGTGTTT 1157
Db 1247 aggtagatgcagaaaattgctctaaagagagacc 1282
QY 1158 AGGTAGATGCAGAAAATTGCTTAAGAGGAAGGACC 1193

RESULT 5
ID T85162 standard: cDNA; 1915 BP.

AC T85162;
DT 14-DEC-1997 (first entry)
DE Human chemokine receptor 88-2B cDNA.
KW Chemokine receptor 88-2B; atherosclerosis; rheumatoid arthritis;
tumour; asthma; viral infection; AIDS; inflammation;
KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
KW G protein coupled receptor; human; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 362..1429 /*tag= a

PN WO9722698-A2.
PD 26-JUN-1997.
PF 20-DEC-1996; U20759.
PR 07-JUN-1996; US-661393.
PR 20-DEC-1995; US-575967.
PA (ICOS-) ICOS CORP.
PI Gray PW, Raport CJ, Schweickart VL;
DR WPI; 97-341689/31.
DR P-PSDB; W27124.
PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used
to modulate leukocyte trafficking, e.g. for treatment of
PT inflammation, tumours, viral infections, autoimmune diseases, etc.
PS Claim 7; Page 48-50; 65pp; English.
CC This sequence comprises a full-length cDNA coding for novel human
chemokine receptor 88-2B (W27124), a G protein coupled receptor that
is involved in leukocyte trafficking. The 88-2B cDNA was obtained
CC from a macrophage cDNA library using 88-2B-specific primers. A
CC full-length clone (see T89161) for chemokine receptor 88C (W27123)
CC was also obtained. 88C and 88-2B cDNAs can be used to produce
CC recombinant polypeptides in transformed host cells for use in the
CC treatment of e.g. atherosclerosis, rheumatoid arthritis, tumours,
CC asthma, viral infection, AIDS and inflammatory conditions. Nucleic
CC acid fragments can be used to isolate genomic sequences, to detect
CC alleles of the gene (for diagnosis or in gene therapy), to alter
CC receptor genetics to facilitate identification of modulators and to
CC produce knockout animals, and (antisense forms) to alter/study the
CC genetics and expression of the receptor.
SQ Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T;

Query Match 93.0%; Score 1110; DB 34; Length 1915;
Best Local Similarity 99.9%; Pred. No. 0.00e+00;
Matches 1116; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 348 caggggagagtgaaatgacaaactcactagatagatagacaccttgggtaccacatctc 407
QY 78 CAGGGAGAGTGAATGACAACTCCTACTAGATACAGTTGAGACCTTTGGTACCACATCCT 137
Db 408 actatgatcacgtggcgctgctctgtgaaaagctgataccagagcacgtatggccag 467
QY 138 ACTATGATGACGTGGGCCCTGCTCTGTGAAAAAGCTGATACAGAGCACTGATGGCCCACT 197
Db 468 ttgtgccccgcctgtactcctcctggtgttccactgtggccctcttgggcaatgtggtggtg 527
QY 198 TTGTGCCCCGCGTGTACTCCCTGGTGTTCACGTGTGGCCCTCTTGGGCAATGTGGTGTG 257
Db 528 tgatgatcctcataaaataacagagagctccgaattatgaccaaactctacctgctcaacc 587
QY 258 TGATGATCCTCATAAAATACAGAGAGCTCCGAATTTATGACCAACATCTACCTGCTCAACC 317
Db 588 tggccatttcggaccctgtcttctcgttcaaccctccattcttgatccactatgtcaggg 647
QY 318 TGGCCATTTTCGACCTGCTCTTCTCTGTCACCTTCCATTTCTGGATCCACTATGTGAGGG 377
Db 648 ggcataactgggtttttggccatggcatgtgtaagctctcctcagggtttttatcacacag 707
QY 378 GGCATAACTGGGGTTTTTGGCCATGGCATGTGTAAAGCTCTCTCAGGGTTTTTATCACACAG 437
Db 708 gctgttacagcagagatctttttcataatcctcgtcgtgacaatcgacaggttacctggccattg 767
QY 438 GCTGTGACAGCAGATCTTTTTCATATCTCTGCTGACAAATCGACAGGTACCTGCGCCATTG 497
Db 768 tccatcgtgtgttggcccttcgagcccgagctgtcacttttgggtgtcattccaccagcagctg 827

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828 tcacctggggcctggcagctagcagctctctctctgaatttatcttatgagagactgaag 887
Qy      |||||||
558 TCACCTGGGGCCTGGCAGCTGCTAGCAGCTCTCTCTGAAATTTATCTTCTATGAGACTGAAG 617
Db      |||||||
888 agtggttgaagagactcttgagctgctcttaccacagagatacagtatatagctgga 947
Qy      |||||||
618 AGTTGTTTGAAGAGACTCTTTGCACTGCTCTTTACCCAGAGGATACAGTATATAGCTGGA 677
Db      |||||||
948 ggcatttcacactctgagaatgaccattctctgctctgctctctctctctctctctggt 1007
Qy      |||||||
678 GGCATTTCACACTGAGATGACCATCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTTATGG 737
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1008 ccattctgtacacaggaatcatcaaacgctgctgagtgccccagtaaaaaaagtaca 1067
Qy      |||||||
738 CCATCTGTACACAGGAATCATCAAAACGCTGCTGAGTGCCCCCAGTAAAAAAGTACA 797
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1068 aggcacatcggtcattttttgtcatcatcgagggtgtttttcattttctggacacccctaca 1127
Qy      |||||||
798 AGGCCATCCGGCTCATTTTCTCATCATGCGCGTGTCTTTTTCATTTCTGGACACCCCTACA 857
Db      |||||||
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Qy      |||||||
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1428 aggtcagatgagaaaaattgctctaaagaggagacc 1464
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1158 AGGT-AGATGCAGAAAATTGCTTAAGAGGAAGGACC 1193
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RESULT 6

ID T93601 standard; cDNA; 5099 BP.

T93601;

07-MAY-1998 (first entry)

Human eosinophil eotaxin receptor CC CKR3 encoding cDNA.

KW Eosinophil eotaxin receptor; CC CKR3; human; treatment; dermatitis;

KW atopic condition; allergic rhinitis; conjunctivitis; bronchial asthma;

KW beta-chemokine receptor; viral infection; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT misc_feature 1..3586

FT /*tag= a

FT /note= "5' genomic DNA flanking sequence"

FT 3587..4654

FT /*tag= b

FT /product= "human eosinophil eotaxin receptor"

FT 4655..5099

FT /*tag= c

FT /note= "terminator region"

FN W09741154-A1.

PD 06-NOV-1997.

PF 24-APR-1997; U06568.

PR 17-JAN-1997; GB-000894.

PR 26-APR-1996; US-016158.

PR 26-APR-1996; US-017113.

```
PA (MERI ) MERCK & CO INC.
PI Daugherty BL, Demartino JA, Siciliano SJ, Springer MS;
DR WPI; 97-549685/50.
DR P-PSDB; W31850.
PT New isolated human eosinophil eotaxin receptor - used to develop
PT products for treating and preventing atopic conditions e.g. allergic
PT rhinitis, dermatitis, conjunctivitis and bronchial asthma
PS Claims 12, 13, 14; Pages 16-20; 51pp; English.
CC This cDNA encodes a human eosinophil eotaxin receptor. This 5099 base
CC pair sequence comprises a 1065 base pair open reading frame encoding a
CC 355 amino acid eosinophil eotaxin receptor protein, flanked by a 5'
CC genomic DNA sequence and a 3' terminator region. This novel eosinophil
CC eotaxin receptor is a human beta-chemokine receptor designated CC CKR3.
CC Agents which bind to this eosinophil eotaxin receptor can be used for
CC the treatment and prevention of atopic conditions such as allergic
CC rhinitis, dermatitis, conjunctivitis and bronchial asthma. Agents which
CC block this eosinophil eotaxin receptor can be used to prevent viral
CC infection in healthy individuals and slow or halt viral progression
CC in infected patients.
SQ Sequence 5099 BP; 1388 A; 1171 C; 1013 G; 1527 T;
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Query Match 93.0%; Score 1110; DB 38; Length 5099;

Best Local Similarity 99.9%; Pred. No. 0.00e+00;

Matches 1116; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 3633 actatgatgacgtgggctgctctgtgaaaaagctgtaccagagacctgatggcccaagt 3692
Qy 138 ACTATGATGACGTGGGCTGCTCTGTGAAAAAGCTGTATACCAGAGCACTGATGGCCCACT 197
Db 3693 ttgtgccccgcgtgactccctggttccactgtggcctctctgtggcaatgtgtgtg 3752
Qy 198 TTGTGCCCCCGCTGACTCCCTGGTGTCTACTGTGGGCCCTCTTGGGCAATGTGTGTGGTGG 257
Db 3753 tgatgatctctcaataataacacaggggtccgaattatgacaaacatctacctgctcaacc 3812
Qy 258 TGATGATCTCTATAAAATACAGGAGGCTCGAATATATGACCAACATATACCTGCTCAACC 317
Db 3813 tggccatttcggacctctctctctctctctctctctctctctctctctctctctctctctct 3872
Qy 318 TGGCCATTTCCGACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 377
Db 3873 ggcataactgggttttggccatggcagtgtaagctccctcaggggttttatcacacag 3932
Qy 378 GGCATAACTGGGTTTTTGGCCATGGCATGTGTAAAGCTCCTCTCAGGGTTTTATCACACAG 437
Db 3933 gcttgtagcagagatcttttttcaataatcctgctgacaatcgacagtgacctggccattg 3992
Qy 438 GCTTGTACAGCGAGATCTTTTTCATAATCCTGCTGACAAATCGACAGGTACTGTGCCCATTTG 497
Db 3993 tcaatgctgtgttgccctctggagcccgacctgctcaattttgtgtgtcatcacagacatcg 4052
Qy 498 TCCAATGCTGTGTGTGGCCCTTCGAGCCCGAGCTGTACATTTTGTGTGTGTGTGTGTGTGTGT 557
Db 4053 tcacctgggcccctggcagtgctagcagctctctctgaatttatctctctatgagactgaag 4112
Qy 558 TCACCTGGGCGCTGGCAGTCTTCTCTGAAATTTATCTTCTATGAGACTGAAG 617
Db 4113 agttgtttgaagagactcttttgagtgctctttaccacagaggtacacagtatatagctgga 4172
Qy 618 AGTTGTTTGAAGAGACTCTTTGACAGTCTCTTTACCCAGAGGATACAGTATATAGCTGGA 677
Db 4173 ggcatttcacactctgagaatgacacatctctctctctctctctctctctctctctctctct 4232
Qy 678 GGCATTTCCACTCTGAGAAATGACCATCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 737
Db 4233 ccattctgtacacaggaatcatcaaacgctgctgaggtgtccccagtaaaaaaagtaca 4292
Qy 738 CCATCTGCTACACAGGAATCATCAAAACGCTGCTGAGGTGCCCCCAGTAAAAAAGTACA 797
```


KW	macrophage inflammatory protein 1 alpha; diabetes; central disease;	
KW	regulated on activation, normal T cell expressed and secreted; allergy;	
KW	affinity compound; expression vector; CHO cell; viral disease;	
KW	infectious disease; tumour; hyperlipidaemia; hypercholesterolaemia; ss.	
KS	Homo sapiens.	
PN	J09176048-A.	
PD	08-JUL-1997.	
PF	28-DEC-1995; 342130.	
PR	28-DEC-1995; JP-342130.	
PA	(TAKE) TAKEDA CHEM IND LTD.	
DR	WPI; 97-399449/37.	
DR	P-PSDB; W25751.	
PT	Preparation of human MIP-1-alpha/RANTES receptor protein - used in	
PT	the treatment of viral diseases, tumours, allergy, diabetes	
PT	osteoporosis etc.	
PS	Claim 6: Page 15; 19pp; Japanese.	
CC	This sequence encodes human MIP-1 alpha/RANTES receptor (macrophage	
CC	inflammatory protein 1 alpha/regulated on activation, normal T cell	
CC	expressed and secreted). The human MIP-1 alpha/RANTES receptor protein	
CC	may be used in a method for the screening of human MIP-1 alpha/RANTES	
CC	receptor affinity compounds. The MIP-1 alpha/RANTES receptor coding	
CC	sequence may be included in an expression vector, preferably pPCR, and	
CC	used to transform a CHO cell for use in the same method. The receptor	
CC	protein can provide a preventive and treating agent for viral diseases,	
CC	infectious diseases, tumours, allergy, diabetes, central diseases,	
CC	hyperlipidaemia, hypercholesterolaemia, osteoporosis, digestive ulcers,	
CC	etc.	
SO	Sequence 1065 BP; 228 A; 284 C; 253 G; 300 T;	

Query Match	35.9%	Score 428	DB 33	Length 1065
Best Local Similarity	72.2%	Pred. No. 1.28e-295		
Matches	697	Conservative	0	Mismatches 269; Indels 0; Gaps 0
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Qy	190	GGCCACATTTGTGCCCCCGGTGTACTCCCTGGTGTTCACGTGGGCTCTTGGGCAATGT	249	
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Qy	250	GGTGGTGTATGATCCTCATAAATACAGAGGCTCCGAATTATGACCAACATCTACCT	309	
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Qy	310	GCTCAACCTGGCCATTTCCGACCTGCTCTTCCTCGTCACCTTCCCATCTGAGATCCACIA	369	
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Qy	370	TGTCAGGGGGCATAACTGGGTTTTTGCCATGGCATGTGTAACTCCTCTCAGGGTTTA	429	
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Qy	430	TCACACAGGCTGTACAGCGAGATCTTTTTCATAATCCTGCTGACAAATCGACAGTACCT	489	
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Qy	490	GGCCATTGTCAGTCTGTGTTTGCCCTTCGAGCCGGACGTCACTTTTGGTGTCAATCAC	549	
Db	459	cagcatcatctattggggccctggccatcttggcttccatgccaggcttatactttccaa	518	
Qy	550	CAGCATCGTCACTTGGGCGCTGGCAGTCTAGCAGCTCTTCCCTGAATTTATCTTCTATGA	609	
Db	519	gacccaatgggaattcaactcaccacactcagccttcaacttctcacaagaagactaag	578	
Qy	610	GACTTGAGAGTTGTTTGAAGAGACTCTTTGCAGTGTCTTTTACCAGAGGATACAGTATA	669	
Db	579	agagtgaagctgttttcaggctctgaaactgaaaccttttggctggtattgacctttgtt	638	
Qy	670	TAGCTGGAGGCATTTCCCACTCTGAGAATGACCATCTTCTGTCTGCTTCTCCCTCTGCT	729	
Db	639	ggctcatgatcctctgtacacagggatataaagattctctgaagacagacaaatagaa	698	
Qy	730	CGTTATGGCCATCTGCTACACAGGAATCATCAAAACGCTCTGAGTGGCCCGAGTAAAAA	789	

Db	599	gaatccaagctgctgcgtttgattttgtcatcatgatcatctttttctcttttgagc	758
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Db	759	ccctacaattgaactatactattctgttttccaagacttccctgttccacccatgagt	818
Qy	850	ACCTTACAATGTGGCTATCCTTCTCTTCCCTATCAATCCATCTTATTTGGAAATGACTG	909
Db	819	tgagcagagcagacatttgaccctgctgctgaagtgcaggagggtgatcgcctacaagca	878
Qy	910	TGAGCGGAGCAACATCTGGACCTGGTCATGCTGGTGACAGAGGTGATCGCTACTCCCA	969
Db	879	ctgtgtgtcaacccagtgatcatagcccttctgtgtgagagggttcggaagtaacctgcy	938
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Qy	1030	CCACTTCTCCACAGACCATTTGCTATGCATGCCTGGCGAGATACATCCCATTCCTTCCTAG	1089
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Qy	1090	TGAGAGCTGGAAAGAACCAAGCTCTCTCTCTCCATCCACAGACAGCCGGAACTCTAT	1149
Db	1059	tggggtt 1064	
Qy	1150	TGTGTT 1155	

RESULT 9

ID

Q62695 standard; DNA; 1495 BP.

AC

Q62695;

DT

30-JAN-1995 (first entry)

DE

C-C chemokine receptor DNA.

KW

C-C CKR-1; cytokine; inflammation; ds.

OS

Homo sapiens.

PN

W09411504-A.

PF

26-MAY-1994.

PR

04-NOV-1993; U10672.

PA

10-NOV-1992; US-974025.

FI

Horuk R, Neote K, Schall T;

DR

P-PSDB; R52749.

PT

New C-C chemokine receptor and nucleic acid - are used to develop

PT

prods. for use in diagnosis and therapy of inflammation and other

FS

cytokine-mediated disorders

CC

Claim 17; Fig 9; 90pp; English.

CC

The sequence is that of the C-C chemokine receptor gene which was

CC

isolated by PCR from PMA treated HL60 cells using PCR primers whose

CC

sequence was designed to correspond to conserved sequences in two

CC

transmembrane regions of known cytokine receptors. The sequence can

CC

be used in therapeutic or diagnostic compsns. for inflammation and

CC

other cytokine mediated disorders.

SQ

Sequence 1495 BP; 348 A; 389 C; 361 G; 397 T;

Query Match	35.98;	Score 428;	DB 11;	Length 1495;
Best Local Similarity	72.28;	Pred. No. 1.28e-295;		
Matches	697;	Conservative 0;	Mismatches 269;	Indels 0; Gaps

Db	99	ggcccaactgctgccctctgtactcctctgttattgtcattggcctggttgggaacat	158
Qy	190	GGCCCCAGTTGTGCCCGCTGTACTCCCTGGTGTACTGTGGCCCTCTTGGGCAATG	249
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Qy	250	GGTGGTGTGATGATCCTATAAAATACAGAGGGTCCGAATTAATGACCAATCTACCT	309
Db	219	octgaacctggcatttctgacctctcttcttctgttcacgcttccctcttgatcgacta	278
Qy	310	GCTCAACCTGGCAATTCGGACCTGCTCTCTCTCTGTCGCCCTTCATCTGGATCCCA	369
Db	279	caagttgaagatgactgggttttttggatgcatgtgataagatcctctctctgggttta	338

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MUSEUM
(TM)

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ch_p protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Dec 8 13:12:59 1998; Maspar time 14.68 Seconds
Tabular output not generated. 825.479 Million cell updates/sec

Title: >US-08-963-656-2
Description: (1-355) from US08963656.pep
Perfect Score: 2765
Sequence: 1 MTSLDVTEFTGTSYDDV.....LERTSVSPSTAEBELSIIV 355

Scoring table: PAM 150
Gap 11

Searched: 107076 seqs, 34141958 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r56
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 48.857; Variance 137.519; scale 0.355

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2751	99.5	355	2	G02436	C-C chemokine receptor	0.00e+00
2	2729	98.7	355	2	A57237	chemokine (C-C) recep	0.00e+00
3	1874	67.8	359	2	149341	MIP-1 alpha receptor	2.08e-252
4	1828	66.1	355	2	A45177	chemokine (C-C) recep	1.74e-245
5	1717	62.1	355	2	I49339	macrophage inflammo	8.37e-229
6	1497	54.1	352	2	G02653	CC chemokine receptor	7.85e-195
7	1496	54.1	352	2	A43113	chemokine (C-C) recep	1.11e-195
8	1452	52.5	353	2	S55594	G protein-coupled rec	4.19e-189
9	1438	52.0	360	2	JC2443	chemokine (C-C) recep	5.17e-187
10	1433	51.8	356	2	I49340	MIP-1 alpha receptor	2.88e-186
11	1352	48.9	374	2	I38450	chemokine (C-C) recep	3.51e-114
12	1256	45.4	360	2	A57160	chemokine (C-C) recep	6.85e-95
13	1198	43.3	360	2	JC4587	chemokine (C-C) recep	2.81e-151
14	1079	39.0	355	2	JC5067	G protein-coupled rec	1.17e-133
15	1074	38.8	354	2	I58186	hypothetical G-protei	6.42e-133
16	1006	36.4	355	2	JC4304	orphan G-protein-cou	6.85e-123
17	863	31.2	359	2	JC5068	G protein-coupled rec	6.52e-102
18	816	29.5	378	2	B55735	lymphocyte-specific G	4.68e-91
19	787	28.5	378	2	A45680	G protein-coupled pep	7.73e-91
20	767	27.7	378	2	A55735	G protein-coupled pep	6.20e-88
21	738	26.7	360	2	A53611	interleukin-8 recepto	9.88e-84
22	725	26.2	350	2	A39445	interleukin-8 recepto	7.48e-82
23	715	25.9	355	2	JQ1231	interleukin-8 recepto	2.08e-80

24	713	25.8	352	2	A45747	leukocyte-derived sev	4.05e-80
25	704	25.5	352	2	G00048	fusin (LSTR) - crsb	8.06e-79
26	698	25.2	358	2	A53752	interleukin-8 recepto	5.91e-78
27	685	24.8	353	2	S28787	neuropeptide y/peptid	4.41e-76
28	668	24.2	374	2	A42628	G-protein coupled rec	1.23e-73
29	658	23.8	359	2	A42656	angiotensin II recept	3.36e-72
30	652	23.6	350	2	JN0621	G-protein coupled rec	2.44e-71
31	652	23.5	356	2	S42096	interleukin-8 recepto	2.44e-71
32	649	23.5	359	2	A48921	interleukin-8 recepto	6.56e-71
33	647	23.4	359	2	S44425	angiotensin II recept	1.27e-70
34	647	23.4	374	2	S32785	G protein-coupled rec	1.27e-70
35	644	23.3	359	2	JQ1516	angiotensin II recept	3.42e-70
36	643	23.3	359	2	JC2134	angiotensin II recept	6.61e-70
37	642	23.2	359	2	JC1104	angiotensin II recept	6.61e-70
38	638	23.1	327	2	S56162	MDCK15 protein - huma	2.47e-69
39	640	23.1	359	2	JH0621	angiotensin receptor	1.28e-69
40	638	23.1	372	2	S26667	G protein-coupled rec	2.47e-69
41	637	23.0	359	2	A48857	AT1 angiotensin II re	3.44e-69
42	636	23.0	359	2	I51372	angiotensin receptor	4.78e-69
43	634	22.9	359	2	S15403	angiotensin II recept	9.25e-68
44	628	22.7	363	2	JC2543	angiotensin II recept	6.68e-68
45	628	22.7	363	2	JC2435	angiotensin II type 2	6.68e-68

ALIGNMENTS

RESULT 1
ENTRY G02436 #type complete
TITLE C-C chemokine receptor 3 - human
ORGANISM #formal name Homo sapiens #common name man
DATE 21-Dec-1990 #sequence revision 06-Jun-1997 #text change 06-Jun-1997

ACCESSIONS G02436
REFERENCE H01272
#authors Ponath, P.D.
#submission submitted to the EMBL Data Library, February 1996
#accession G02436
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-355 #label PON
#cross-references EMBL:U49727; NID:q1477560; PID:q1477561
SUMMARY #length 355 #molecular-weight 41057 #checksum 477

Query Match 99.5%; Score 2751; DB 2; Length 355;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 354; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	1	MTSLDVTVEFTGTSYDDVGLCKRADRALMAQFVPLYSLVFTVGLGNVVVMI	60
Db	61	KYRRLRIMNTIYLNLALISDLFLVLPFWHYVGHMNVFGHCKLISGFYHTGLYSE	120
Qy	61	KYRRLRIMNTIYLNLALISDLFLVLPFWHYVGHMNVFGHCKLISGFYHTGLYSE	120
Db	121	IFFIILLTDRLAIVHAVFALRARTVFGVTSIVTWGLAVLAALPERIFETEELFEE	180
Qy	121	IFFIILLTDRLAIVHAVFALRARTVFGVTSIVTWGLAVLAALPERIFETEELFEE	180
Db	181	TLCSALYPEDTYVSRNHFITLMTIFCLVPLLVNAICTGTIKTLRCPSSKKKKAIRL	240
Qy	181	TLCSALYPEDTYVSRNHFITLMTIFCLVPLLVNAICTGTIKTLRCPSSKKKKAIRL	240
Db	241	IFVIMAVFIFMTFPVNVAILSSYOSILFGNDCERTKHDLVNLTEVYASHCCMNPVI	300
Qy	241	IFVIMAVFIFMTFPVNVAILSSYOSILFGNDCERTKHDLVNLTEVYASHCCMNPVI	300
Db	301	YAFVGEFRFRKYLRFHFHRLMLHGLRYIPFLDSEKLEKTSVSPSTAEBELSIIV	355
Qy	301	YAFVGEFRFRKYLRFHFHRLMLHGLRYIPFLDSEKLEKTSVSPSTAEBELSIIV	355

ENTRY A57237 #type complete
TITLE Chemokine (C-C) receptor 3 - human
ALTERNATE_NAMES C-C CKR-3
ORGANISM #formal_name Homo sapiens #common_name man
DATE 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change
29-Aug-1997
ACCESSIONS A57237
REFERENCE A57237
#authors Combadierre, C.; Ahuja, S.K.; Murphy, P.M.
#journal J. Biol. Chem. (1995) 270:16491-16494
#title Cloning and functional expression of a human eosinophil CC
chemokine receptor.
#accession A57237
#status preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-355 #label COM
#cross-references GB:028694
GENETICS
#gene GDB:CMKBR3
##cross-references GDB:579624; OMIM:601268
#map_position 3p21-3p21
#remarks 6 protein-coupled receptor; glycoprotein; phosphoprotein;
transmembrane protein
#RE
36-60 #domain transmembrane #status predicted #label TM1\
71-91 #domain transmembrane #status predicted #label TM2\
108-129 #domain transmembrane #status predicted #label TM3\
147-171 #domain transmembrane #status predicted #label TM4\
205-223 #domain transmembrane #status predicted #label TM5\
240-261 #domain transmembrane #status predicted #label TM6\
268-305 #domain transmembrane #status predicted #label TM7\
24-272,106-183 #disulfide_bonds #status predicted\
345 #binding_site phosphate (Ser) (covalent) (by casein
kinase II) #status predicted
SUMMARY #length 355 #molecular_weight 41072 #checksum 897
Query Match 98.74; Score 2729; DB 2; Length 355;
Best Local Similarity 98.9%; Pred. No. 0.00e+00;
Matches 351; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 1 MTSLSDTVEFTGTSYDDVGLLCEKADTRALMAQFVPLYSIVFTVGLGNVVMILI 60
QY 1 MTSLSDTVEFTGTSYDDVGLLCEKADTRALMAQFVPLYSIVFTVGLGNVVMILI 60
Db 61 KRRRLRIMNITLLNLAISDLFLVLPFWIHVYRGHNWFGHGMCKNLGFTYHGLYSE 120
QY 61 KRRRLRIMNITLLNLAISDLFLVLPFWIHVYRGHNWFGHGMCKNLGFTYHGLYSE 120
Db 121 IFFIILLTDRILAIYHVAEVALRARTVETGVTSTVWGLAVLAALPEFIETETELFEE 180
QY 121 IFFIILLTDRILAIYHVAEVALRARTVETGVTSTVWGLAVLAALPEFIETETELFEE 180
Db 181 TLCSALYPEDYVYSMRHFRTLRKTFCLVPLVMAICYTGIIKTLRCPKSKKYYAIRL 240
QY 181 TLCSALYPEDYVYSMRHFRTLRKTFCLVPLVMAICYTGIIKTLRCPKSKKYYAIRL 240
Db 241 IIVYIAVAFIETFPYVVALLSYOSILFGNDCERKHLDRVAVLYEVAISHCCNPYI 300
QY 241 IIVYIAVAFIETFPYVVALLSYOSILFGNDCERKHLDRVAVLYEVAISHCCNPYI 300
Db 301 YAFVGERFRKYLRFHFRHLMLGRIYFPLPSEKLEKRTSSVSPSAEDELIVF 355
QY 301 YAFVGERFRKYLRFHFRHLMLGRIYFPLPSEKLEKRTSSVSPSAEDELIVF 355
RESULT 3
ENTRY 149341 #type complete
TITLE MIP-1 alpha receptor like-2 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
28-Feb-1997
ACCESSIONS 149341
REFERENCE 149341

#authors Gao, J.L.; Murphy, P.M.
#journal J. Biol. Chem. (1995) 270:17494-17501
#title Cloning and differential tissue-specific expression of three
mouse beta chemokine receptor-like genes, including the
gene for a functional macrophage inflammatory protein-1
alpha receptor.
#cross-references MUID:95340546
#accession I49341
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-359 #label RBS
#cross-references EMBL:U28406; NID:9881551; PID:9881552
SUMMARY #length 359 #molecular_weight 41857 #checksum 8333
Query Match 67.8%; Score 1874; DB 2; Length 359;
Best Local Similarity 68.5%; Pred. No. 2.08e-252;
Matches 239; Conservative 50; Mismatches 58; Indels 2; Gaps 2;
Db 12 VESFETPEYEMAMP-CEKVRKEIGSMILPPLYSIVFTIIGLGNMNVYLIRKRLQ 70
QY 8 VETFGTISTY-IDVGLLCEKADTRALMAQFVPLYSIVFTIIGLGNVVMILIKRRLR 66
Db 71 IMTNLYLNLALISDLFLFTVPFWIHVYLMNMGFGHYMCKMLSGFYIALYSEIFITL 130
QY 67 IMTNLYLNLALISDLFLVLPFWIHVYRGHNWFGHGMCKNLGFTYHGLYSEIFITL 126
Db 131 LTIDRYLAIVAVRLARVTFATITSITWGLAGLAALPEFIETETELFEE 186
QY 127 LTIDRYLAIVAVRLARVTFATITSITWGLAGLAALPEFIETETELFEE 186
Db 191 YPEGSDMKRPFHALRMNIFGALPLVAVNVCYSGIITLRCNKKKRIIRLIFVMI 250
QY 187 YPEDVIVYMRHFRHTLRMTIFCLVLPVMAICYTGIIKTLRCPKSKKYYAIRLIFVMA 246
Db 251 VEFIFWTPYNNVLLFSAPHSFLETSCEQSKHLDLMAQVETVATVHCCVNPVYAEVGE 310
QY 247 VEFIFWTPYNNVLLFSAPHSFLETSCEQSKHLDLMAQVETVATVHCCVNPVYAEVGE 306
Db 311 RFRKRLRFPHRNQVTFENITFQPLPGENGRITSSVSTGEDELIVF 359
QY 307 RFRKRLRFPHRNQVTFENITFQPLPGENGRITSSVSTGEDELIVF 355
RESULT 4
ENTRY A45177 #type complete
TITLE Chemokine (C-C) receptor 1 - human
ALTERNATE_NAMES C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
10-Sep-1997
ACCESSIONS A45177; I55671
REFERENCE A45177
#authors Neote, K.; Digregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
#journal Cell (1993) 72:415-425
#title Molecular cloning, functional expression, and signaling
characteristics of a C-C chemokine receptor.
#cross-references MUID:93161416
#accession A45177
#status nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-355 #label NEO
#cross-references GB:LI0918; NID:9292416; PID:9292417
#experimental_source HL60 cells
#note Sequence extracted from NCBI backbone (NCBIP:124876)
REFERENCE I55671
#authors Gao, J.
#journal J. Exp. Med. (1993) 177:1421-1427
#title Structure and functional expression of the human macrophage
inflammatory 1 alpha (MIP-1alpha)/RANTES receptor.
#cross-references MUID:93240122
#accession I55671
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA

GENETICS	FEATURE	RESULTS	REFERENCES
<p>##residues 1-355 ##label RES</p> <p>##cross-references GB:L10918; NID:g292416; PID:g292417</p> <p>#gene GDB:CMKBRL; CMKR-1</p> <p>##cross-references GDB:I38446; OMIT:601159</p> <p>#map_position 3p21-3p21</p> <p>KEYWORDS disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein</p>	<p>36-60 #domain transmembrane #status predicted #label TM1</p> <p>71-91 #domain transmembrane #status predicted #label TM2</p> <p>108-129 #domain transmembrane #status predicted #label TM3</p> <p>147-171 #domain transmembrane #status predicted #label TM4</p> <p>205-223 #domain transmembrane #status predicted #label TM5</p> <p>240-264 #domain transmembrane #status predicted #label TM6</p> <p>288-305 #domain transmembrane #status predicted #label TM7</p> <p>#binding_site carboxylate (Asn) (covalent) #status predicted</p> <p>#disulfide_bonds #status predicted</p> <p>#binding_site phosphate (Ser) (covalent) (by casein kinase II) #status predicted</p>	<p>RESULT 5</p> <p>ENTRY 149339</p> <p>TITLE macrophage inflammatory protein-1 alpha receptor - mouse</p> <p>ORGANISM Mus musculus #common_name mouse</p> <p>DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1996</p> <p>ACCESSIONS I49339</p> <p>REFERENCE I49339</p> <p>Authors Gao, J. L.; Murphy, P. M.</p> <p>#journal J. Biol. Chem. (1995) 270:17494-17501</p> <p>#title Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.</p> <p>#cross-references MIM:95340546</p> <p>#accession I49339</p> <p>#status DNA</p> <p>#molecule_type pre-mRNA</p> <p>#residues 1-355 #label RES</p> <p>##cross-references EMBL:U28404; NID:g881547; PID:g881548</p> <p>##residues 1-355 #molecular_weight 40869 #checksum 6271</p>	<p>SUMMARY</p> <p>Query Match 66.1%; Score 1828; DB 2; Length 355;</p> <p>Best Local Similarity 62.7%; Pred. No. 1.74e-245;</p> <p>Matches 224; Conservative 68; Mismatches 61; Indels 4; Gaps 4;</p>

Query Match	62.1% Score 1717; DB 2; Length 355;
Best Local Similarity	58.1% Pred. No. 8,37e-229;
Matches 207; Conservative	83; Mismatches 64; Indels 2; Gaps 2;
Db 1	MEIS-DEFEAPPTTDEDYDSDTPCOKTAVARACGAGLPLPSLVEIGVGNVLIVL 59
Qy 1	MTSLDLYVEHFGTTSYD-DVGLCEKADTRALMAQVPPVLSVTFPGILGNVVVMTL 59
Db 60	MOHRLOSMTSYLFENLASDLYFLFPWIDYKLDKDMIFGDAMCKLISGYTGLYS 119
Qy 60	IKYRLRLMTNITYLNLDAISDLFLVTLPPFWIHVYGHNMNVEFGHGMCKLISGYHTGLS 119
Db 120	EIEFIIILTDRIYAIAVHAFARARVTLGIIITSITMALATLAMPALPEKAMQMT 179
Qy 120	EIEFIIILTDRIYAIAVHAFARARVTLGIIITSITMALATLAMPALPEFIEPEL 179
Db 180	HRTSPHPYKSLQMKRFQALKNLGLILPLVIMTICAGIIRILRRSEKKAKAVR 239
Qy 180	ETLCSALYEDPTVSWRHFTLRITFCVLPLLVMAICVTGIIITKLRRPSKKYKAR 239
Db 240	LIFATLLFLMTPYLVSFVSAFDVLTNOCBOSKHLDLAMQYEVYATYHCCVNI 299
Qy 240	LIFIMAVFEFTMPYVVALISYOSILEFGNCERTKHLDLAMYTEVYAVASHCCMNV 299
Db 300	IYVVGGERFMYLQOLFQRYAIPALPELISDQLEERTISISPSNGEHSAGF 355
Qy 300	IYAVGERFRKYLHNFHRLHMLHGLKIFPLPSSEKIERISVSPSTAPELSIVF 355
RESULT	6
ENTRY	G02653
TITLE	CC chemokine receptor 5 - human
ORGANISM	#formal_name Homo sapiens #common_name man
DATE	21-Dec-1990 #sequence_revision 06-Jun-1997 #text_change 06-Jun-1997
ACCESSIONS	G02653
REFERENCE	H01541
#authors	Combaldiere, C.
#submission	submitted to the EMBL Data Library, May 1996
#accession	G02653
#status	preliminary; translated from GB/EMBL/DBJ
#molecule	1-mRNA
#residues	1-352 #label COM
#cross-references	EMBL:U57840; NID:q1373407; PID:q1373408
SUMMARY	#length 352 #molecular_weight 40566 #checksum 7048
Query Match	54.1% Score 1497; DB 2; Length 352;
Best Local Similarity	54.3% Pred. No. 7.68e-196;
Matches 182; Conservative	89; Mismatches 55; Indels 9; Gaps 9;
Db 20	COKINWQIARLLPPLYSLVITGFGANMLVILINLCRLKSMYDIYLNLAISDLF 79
Qy 24	CEKADTRALMAQVPPVLSVTFPGILGNVVVMTLKYRLMTNITYLNLDAISDLF 83
Db 80	LIVPFAHVAIAAO-WPFGNTMCLLGLYFIFGFSGIFIIILTDRIYAAVHAFALR 138
Qy 84	LIVLPFWHIVRGNNWFGHGMCKLSGFIHTGLYSIFIIILTDRIYAIAVHAFALR 143
Db 139	ARVTFEGVYVITWVAVAPASLPGLIIFTRSQEGEGLHT-CSSHFPYSQ-YQFWKNFQTL 196
Qy 144	ARVTFEGVYVITWVAVAPASLPGLIIFTRSQEGEGLHT-ELFEETLCSALYEDPTVYS-WRHFTL 201
Db 197	KIVIGLIVLPLLVNIVCSGIIKTLKCRNEKKRRAVRLPFIIMTYVFLMAPYVILL 256
Qy 202	KMTIFCLVPLLVMAICTGTGIIKTLRCPK-KKKYKIRLIFIMAVFEFTMPYVVALI 260
Db 257	LNTFOE-FGLGNSSNRLDOAQVYETLGMTHCCNPIITVAFVGEKFNLYLVFEOKH 315
Qy 261	LSSVQSLIFG-NODEKRKHLDVLAIVTEVYAVASHCCMNPITYAFVGERFRKYLHNFHHR 319
Db 316	IAKRFCKCSIFQOADEPRASSVYTRSTGEOEISV 350
Qy 316	IAKRFCKCSIFQOADEPRASSVYTRSTGEOEISV 350

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Query Match      52.5%; Score 1452; DB 2; Length 383;
Best Local Similarity 54.28; Pred. No. 4,196-189;
Matches 173; Conservative 70; Mismatches 74; Indels 2; Gaps 2

Db      56 YEESAP-CYSQSDTRAAQVPAFLALVLEFGILGNLIVITVIRYKIKNTMLNLN 114
      17 YDDGGLCEKADRIALMAQVFPPLISVFTGSLGNVYVWMLIKYRLIMINILNL 76
Db      115 AISDLFLTLTPFWMHYIGMYHDMTFGSLCKLKGVCYMSYQVFCITLLTVDRYLAV 174
      77 AISDLFLTLVLPFWIHVY-RGNHWVFGHGMCCKLLSGEYHNTGLYSEIFILLTIDRYLAI 135
Db      175 VYAATLAREFTVCGIVTCVCMFAGLLSLPEPEFHODNORNOCDDEYEMSTNW 234
      136 VHAVFARATVATFVGVITSVTWGLAVLAAPLPEFTLEETEELCSALYEDDVYSW 195
Db      235 RRAHVAKIVMLSLTLILIMACYVVIIRRLRBRPSKKYKAAILFIVAVAFVFWTPY 294
      196 RHFTFLMTFTCLVLPFLMALCYGIIKTLRCPSSKKRYAAILFIVIMAVFIFWTY 255
Db      295 NIVLLSTFPAHLNLQCALSSNLMALLITKRYATVHCCINPYIYAVGEKFRRLHYR 354
      256 NVALITSSYQSILFGNDCERTKHLDLVMLETVIAYSHCCKNPYIYAVGEKFRRLHYR 315
Db      355 FHRTVAIYLCKYIPFLSGD 373
      316 FHRLLMHGRIYIPFLPSE 334

RESULT      9
ENTRY      JC2443 #type complete
TITLE      chemokine (C-C) receptor 2, splice form B - human
ALTERNATE_NAMES      C-C-CR2; monocyte chemoattractant protein 1 receptor;
                      monocyte chemotactin 1 receptor
ORGANISM      #formal name Homo sapiens #common name man
DATE      21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change
                      10-Sep-1997
ACCESSIONS      JC2443; 138463
REFERENCE      JC2443
#authors      Yamaegami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
#journal      Biochem. Biophys. Res. Commun. (1994) 202:1156-1162
#title      cDNA cloning and functional expression of a human monocyte
                      chemoattractant protein 1 receptor.
#accession      JC2443
#molecule_type      mRNA
#residues      1-360 #label YAM
#cross-references      DDBJ:D29984; NID:g531246; PID:d1006817; PID:g561247
REFERENCE      A53477
#authors      Charo, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly,
                      A.J.; Coughlin, S.R.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756
#title      Molecular cloning and functional expression of two monocyte
                      chemoattractant protein 1 receptors reveals alternate
                      splicing of the carboxyl-terminal tails.
#cross-references      EMBL:94195821
#accession      I38463
#molecule_type      preliminary
#status      1-360 #label RES
#cross-references      GDB:337364; OMIM:601267
#map_position      3p21-3p21
KEYWORDS      alternative splicing; G protein-coupled receptor;
                      glycoprotein; transmembrane protein

FEATURE
43-70      #domain transmembrane #status predicted #label TM1\
81-100      #domain transmembrane #status predicted #label TM2\
115-136      #domain transmembrane #status predicted #label TM3\
154-178      #domain transmembrane #status predicted #label TM4\
207-226      #domain transmembrane #status predicted #label TM5\
244-268      #domain transmembrane #status predicted #label TM6\

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287-309 #domain transmembrane #status predicted #label TM\
14 #binding site carbohydrate (Asn) (covalent) #status
113-190 #disulfide_bonds #status predicted
SUMMARY #length 360 #molecular-weight 41063 #checksum 1732

Query Match 52.0%; Score 1438; DB 2; Length 360;
Best Local Similarity 53.4%; Pred. No. 5,17e-187;
Matches 183; Conservative 87; Mismatches 63; Indels 10; Gaps 8;

Db 21 TTFEDYDYGAPCHKFDVQIGAOQLPRLYSLVIFGFGNMLVLLINCKKLCITDIY 80
14 TSYXD-DVGLCEKADPTALMAQFVPLYSLVFTFGLLGVVVVIMLKRRRLRIMTNY 72
QY 14 TSYXD-DVGLCEKADPTALMAQFVPLYSLVFTFGLLGVVVVIMLKRRRLRIMTNY 72

Db 81 LNLALSDLLFLTLPLMASHA-ANEMVFGNACKLEFTGLYHIGYGGIFITLITDRY 139
73 LNLALSDLLFLTLPLMASHA-ANEMVFGNACKLEFTGLYHIGYGGIFITLITDRY 132

Db 140 LAIVHAFALKARTVFGVTSVITMLVAFAVSPGIIFFKCKEDSVVYCGPYFP--R- 196
133 LAIVHAFALKARTVFGVTSVITMLVAFAVSPGIIFFKCKEDSVVYCGPYFP--R- 192

Db 197 -GMNHFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRRAVFIITIMYELF 255
193 YSMRHFHTLMRTFCLVPLLVMAICYTGILKTLRCP- KKKYKARLIFVIMAVFIIF 251

Db 256 WTPYNYVILINTQER- FGLSNCESTSQLDAQVETLGMTCCINPIIYAFVGEKFR 314
252 WTPYNYVILINTQER- FGLSNCESTSQLDAQVETLGMTCCINPIIYAFVGEKFR 310

Db 315 YLSVFFRKHTTRKRCQCPYFRETVDGVSTMTSPGDEVS 357
311 YLNFHFRLHMLHGRITPLPSEKLE-RTSVSPSTAPPELS 352

RESULT 10
ENTRY 149340 #type complete
TITLE MIP-1 alpha receptor like-1 - mouse
ORGANISM Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Feb-1997

ACCESSIONS 149340
REFERENCE 149339

#journal J. Biol. Chem. (1995) 270:17494-17501
#title Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.
#cross-references MIM:95340546
#accession 149340
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-356 #label RES
#cross-references EMBL:U28405; NID:9881549; PID:9881550
SUMMARY #length 356 #molecular-weight 40934 #checksum 563

Query Match 51.8%; Score 1433; DB 2; Length 356;
Best Local Similarity 52.0%; Pred. No. 2,88e-186;
Matches 173; Conservative 78; Mismatches 80; Indels 2; Gaps 2;

Db 22 GLFCESINRAFGITVPTPLYSLVFIIGVGHVLLVLIQHRKLRNMTSYFENALSD 81
21 GLFCESINRAFGITVPTPLYSLVFIIGVGHVLLVLIQHRKLRNMTSYFENALSD 80

Db 82 LVFLSTLPFVNDYIMKGMDFGNACKFVSGEYLLIGYSMEFIIITLITDRYLAHVAF 141
81 LVFLSTLPFVNDYIMKGMDFGNACKFVSGEYLLIGYSMEFIIITLITDRYLAHVAF 140

Db 142 ALBARVTFGIISITWVLAALVSPICLVF- KSQMEFVHTCRALILPKSLIRLFRQ 200
141 ALBARVTFGIISITWVLAALVSPICLVF- KSQMEFVHTCRALILPKSLIRLFRQ 199

Db 201 ALTMNIGILPLAMITCYTRINLVHRRPNKKAKVRLIFVITLPLAPYYLAA 260
200 TLMRTFCLVPLLVMAICYTGILKTLRCPKRRKARLIFVIMAVFIITPVNAI 259

Db 261 FVSAPEDVFTFSCLSQOVDLSIMTEALATYHCCVNPVIVGVGRKRYLMQFRH 320
260 LLSYSIILFGNDCETKHLDMVLVTEVIANSHCCMNPVIAFVGERRKRLRHFH 319

Db 321 TAITLPQMLPFLSEDRASARLPSTVEIEMTS 353
320 LTMHLGRYIPLPSEKLERTSSVSPSTAPPELS 352

RESULT 11
ENTRY 138450 #type complete
TITLE chemokine (C-C) receptor 2, splice form A - human
ALTERNATE_NAMES C-C CKR-2; monocyte chemoattractant protein 1 receptor;
ORGANISM monocyte chemoattractin 1 receptor
#formal_name Homo sapiens #common_name man
DATE 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 29-Aug-1997

ACCESSIONS 138450
REFERENCE A53477

#authors Charo, I.F.; Myers, S.U.; Herman, A.; Franci, C.; Connolly, A.D.; Coughlin, S.R.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756
#title Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.
#cross-references MIM:94195821
#accession 138450
#status preliminary
#molecule_type mRNA
#residues 1-374 #label RES
#cross-references EMBL:U03882; NID:9472555; PID:9472556

GENETICS GDB:CKBR2
#gene
#cross-references GDB:337364; OMIM:601267
#map_position 3p21-3p21
KEYWORDS alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

FEATURES
44-68 #domain transmembrane #status predicted #label TM1\
79-99 #domain transmembrane #status predicted #label TM2\
115-136 #domain transmembrane #status predicted #label TM3\
154-178 #domain transmembrane #status predicted #label TM4\
208-226 #domain transmembrane #status predicted #label TM5\
244-265 #domain transmembrane #status predicted #label TM6\
292-309 #domain transmembrane #status predicted #label TM7\
14 #binding site carbohydrate (Asn) (covalent) #status predicted

32-277,113-190 #disulfide_bonds #status predicted
SUMMARY #length 374 #molecular-weight 41914 #checksum 5414

Query Match 48.9%; Score 1352; DB 2; Length 374;
Best Local Similarity 56.2%; Pred. No. 3,51e-174;
Matches 168; Conservative 72; Mismatches 50; Indels 9; Gaps 7;

Db 21 TTFEDYDYGAPCHKFDVQIGAOQLPRLYSLVIFGFGNMLVLLINCKKLCITDIY 80
14 TSYXD-DVGLCEKADPTALMAQFVPLYSLVFTFGLLGVVVVIMLKRRRLRIMTNY 72

Db 81 LNLALSDLLFLTLPLMASHA-ANEMVFGNACKLEFTGLYHIGYGGIFITLITDRY 139
73 LNLALSDLLFLTLPLMASHA-ANEMVFGNACKLEFTGLYHIGYGGIFITLITDRY 132

Db 140 LAIVHAFALKARTVFGVTSVITMLVAFAVSPGIIFFKCKEDSVVYCGPYFP--R- 196
133 LAIVHAFALKARTVFGVTSVITMLVAFAVSPGIIFFKCKEDSVVYCGPYFP--R- 192

Db 197 -GMNHFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKRRRAVFIITIMYELF 255
193 YSMRHFHTLMRTFCLVPLLVMAICYTGILKTLRCP- KKKYKARLIFVIMAVFIIF 251

[illegible]

QY	243	VITAVFLEFMPYVALLISYSQILFNGDCERKHLDMVLTEVIATSHCCMNPVITA	302
Db	306	FLGEEKFRYLIQLFKTRGFLVLCQYGLLIQIYSADTPSSSYOSTWHDH	356
QY	303	FVGEFRKRLRHFFHR-HLMLHGRITPFLPSEKLE-RTSSVSPSTAEPL	351
RESULT	13		
ENTRY	JC4587	#type complete	
TITLE	chemokine (C-C) receptor 4 - mouse		
ORGANISM	formal name Mus musculus #common_name house mouse		
DATE	08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 12-Dec-1997		
ACCESSIONS	JC4587		
REFERENCE	JC4587		
#authors	Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.		
#journal	Power, C.A.		
#title	Biochem. Biophys. Res. Commun. (1996) 218:337-343		
#accession	Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human CC CKR-4.		
##molecule_type	JC4587		
##residues	1-360	#label HOO	
##cross-references	EMBL:X00662; NID:g1167851; PID:e195632; PID:g1167852		
##experimental_source	thymus		
#gene	cc ckr-4		
KEYWORDS	glycoprotein; phosphoprotein; receptor; thymus		
FEATURE	2,183,194		
72,202,350	#binding_site carbohydrate (Asn) (covalent) #status predicted\		
145	#binding-site phosphate (Ser) (covalent) (by casein kinase II) #status predicted\		
321	#binding site phosphate (Ser) (covalent) (by protein kinase C) #status predicted\		
SUMMARY	#binding-site phosphate (Thr) (covalent) (by protein kinase C) #status predicted		
	#length 360 #molecular-weight 41462 #checksum 7852		
Query Match	43.3%; Score 1198; DB 21; Length 360;		
Best Local Similarity	43.7%; Pred. No. 2,81e-151;		
Matches 150; Conservative 92; Mismatches 97; Indels 4; Gaps 4;			
Db	16 YNSYFYESMCKPCTKEGKAFGEVFLPPYSLVFLGLFGNSVYVLYLPEKRLKSMID 75		
QY	11 FGTISYDQVLLCEKADTRALMAQFPLPLXSVLFTGGLGNVYVAILIKYRLKRMIN 70		
Db	76 VYLLNLASIDLLFVLSLPFWGYYAADQ-WFEGGLCKIVSMYLVGSGIFIMMSID 134		
QY	71 IYLLNLASIDLLFVLTPLFPWIMHYRGHNWVGHOMCKLISGFYHTGYSIEIFILLTID 130		
Db	135 RYLAIVAHVPELKLKRLTLGYITSLTIVSAVVRASPLGLLFSTCYTEHNTYCKTOYSVA 194		
QY	131 RYLAIVAHVPELKLKRLTLGYITSLTIVSAVVRASPLGLLFSTCYTEHNTYCKTOYSVA 190		
Db	195 ST-TWKVYLSSEINVLGLIPLGLIMLFWMSIITFTLOCHNEKKNNRVRIRFVVVLFLG 253		
QY	191 TVYSKRHHHTLRMTIFGLVPLPLMALCYGIITKLTRCSKKRYAIRLIFVIMAVFLI 250		
Db	254 FWTPTVNVVLETLVELEVDQCTLEERYLDYAIOATETTLGFIHCCINPVIYFLGKEFKR 313		
QY	251 FWTPTVNVVLETLVELEVDQCTLEERYLDYAIOATETTLGFIHCCINPVIYFLGKEFKR 310		
Db	314 YITQLFRTCRGRLVLCCKHDFLOAYSSADMSSSYTOSTVVDHF 356		
QY	311 YLRHFFHR-HLMLHGRITPFLPSEKLERISSV-SPSTAEPL 351		
RESULT	14		
ENTRY	JC5067	#type complete	
TITLE	G protein-coupled receptor CKR-L1 - human		
ORGANISM	chemokine receptor-like protein TER1; GPR-CY6		
	#formal name Homo sapiens #common name man		

DATE 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 10-Sep-1997

ACCESSIONS JC0567; G02776; G02387

REFERENCE JC067

#authors Zabailos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

#journal Biochem. Biophys. Res. Commun. (1996) 227:846-853

#title Molecular cloning and RNA expression of two new human chemokine receptor-like genes.

#accession JC0567

#molecule_type DNA

#residues 1-355 #label ZAB

##cross-references EMBL:Z79782; NID:91668735; PID:e264772; PID:91668736

REFERENCE H01714

#authors Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.

#submission submitted to the EMBL Data Library, June 1996

#accession G02776

#status translated from GB/EMBL/DBD

##molecule_type DNA

#residues 1-355 #label NAP

##cross-references EMBL:U62556; NID:91468978; PID:91468979

REFERENCE H01154

#authors Bonner, T.I.

#submission submitted to the EMBL Data Library, January 1996

#accession G02387

#status preliminary; translated from GB/EMBL/DBD

##molecule_type DNA

#residues 1-355 #label BON

##cross-references EMBL:U45983; NID:91245057; PID:91245057

COMMENT This protein belongs to the family of beta chemokine receptors.

GENETICS

KEYWORDS TER1

FEATURES

36-63 G protein-coupled receptor; transmembrane protein

73-94

108-129

147-171

200-222

239-260

281-304

SUMMARY

Query Match 39.0%; Score 1079; DB 2; Length 355;

Best Local Similarity 39.1%; Pred. No. 1.17e-133;

Matches 133; Conservative 97; Mismatches 102; Indels 8; Gaps 6;

RESULT 15

ENTRY IS8186 #type complete

TITLE hypothetical G-protein coupled receptor - rat

ORGANISM #normal_name Rattus norvegicus #common_name Norway rat

DATE 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 30-May-1997

ACCESSIONS IS8186

REFERENCE IS8186

#authors Harrison, J.K.; Barber, C.M.; Lynch, K.R.

#journal Neurosci. Lett. (1994) 169:85-89

#title CDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and brain related to chemokine receptors.

##cross-references MIMD:94323113

#accession IS8186

#status preliminary; translated from GB/EMBL/DBD

##molecule_type mRNA

#residues 1-354 #label RES

##cross-references EMBL:U04808; NID:9439860; PID:9439861

KEYWORDS G protein-coupled receptor

SUMMARY #length 354 #molecular-weight 40327 #checksum 4478

Query Match 38.8%; Score 1074; DB 2; Length 354;

Best Local Similarity 45.2%; Pred. No. 6.42e-133;

Matches 140; Conservative 77; Mismatches 88; Indels 5; Gaps 4;

Search completed: Tue Dec 8 13:14:00 1998

Job time : 61 secs.

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QY 303 FVGEFRFRYLRHFRHRLHMLGRYIFLPSEKERTSSVSPSTAPELSTVF 355

RESULT 2 PRELIMINARY; PRT; 359 AA.

ID 054814; PRELIMINARY; PRT; 359 AA.

AC 054814; PRELIMINARY; PRT; 359 AA.

DT 01-JUN-1998 (TREMBLREL. 06, CREATED)

DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)

DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)

DE CHEMOKINE RECEPTOR CCR3.

OS RATTUS NORVEGICUS (RAT).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

RN EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-WISTAR; TISSUE-SPLEEN;

RA JIANG Y., SALAFRANCA M.N., ADHIKARI S., XIA Y., FENG L., SONNTAG M.K.,

RA DELEBE C.M., PENNELL N.A., STREET W.J., HARRISON J.K.,

RA J. NEUROIMMUNOL. 0:0-0(1998).

DR EMBL: AF003954; G2897073; .

SO SEQUENCE 359 AA; 41643 MW; C1PC7OCA CRC32;

Query Match 69.8%; Score 1926; DB 11; Length 359;

Best Local Similarity 68.8%; Pred. No. 2,35e-275;

Matches 243; Conservative 55; Mismatches 52; Indels 3; Gaps 3;

DB 8 LKTVETETTYEYEWAPP-CEKVSIRRLGSLWLLPPLYSLVFVGLGNMNVLLIKY 66

QY 5 LDTV-ETFGTYSY-YDDVGLCEKADTRALMAQFVPPLYSLVFVGLGNMNVLLIKY 62

DB 67 RRLQMTNTNYLNLASDLFLFTVFPFMYHYLMNMGHGMCKMISGLYLYLALYSEIF 126

QY 63 RRLRMTNTNYLNLASDLFLFTVFPFMYHYRGNHMGHGMCKMISGLYLYLALYSEIF 122

DB 127 FILLLTDIRYLAIVAVLALRATYTFATITSIITMGFAVLAALDEFFIESODNFGDLS 186

QY 123 FILLLTDIRYLAIVAVLALRATYTFATITSIITMGFAVLAALDEFFIESODNFGDLS 182

DB 187 CSPPRPEGEEDSKRFFHALRMNIFGLAPLLMIVICYSIGIITLLRCPNKKHKAIOLEIF 246

QY 183 CSALPEDETVVSWRHFHRLMTIFCLVPLVMAICYGIIKTLLRCPNKKHKAIRLIF 242

DB 247 VMVIEFTEFMPYNYLVLLSAFHSFLETSQOOSHLDLAMVTEVITHHCCINPIIYA 306

QY 243 VIMAEFFTEFMPYNYLVLLSAFHSFLETSQOOSHLDLAMVTEVITHHCCINPIIYA 302

DB 307 FVGEFRFRYLRHFRHRLHMLGRYIFLPSEKERTSSVSPSTAPELSTVF 359

QY 303 FVGEFRFRYLRHFRHRLHMLGRYIFLPSEKERTSSVSPSTAPELSTVF 355

Query Match 54.2%; Score 1495; DB 6; Length 352;

Best Local Similarity 55.2%; Pred. No. 7,95e-207;

Matches 185; Conservative 84; Mismatches 57; Indels 9; Gaps 9;

DB 20 COKINGQIARLLPPLYSLVFVGNILVLLINCKRKSMTDIYLLNLASDLF 79

QY 24 CEKADTRALMAQFVPPLYSLVFVGLGNMNVLLIKYRRLMTNTNYLNLASDLF 83

DB 80 LLTPPEFAHYAAAO-WDEGNTMCOLLGLYFIFGSGIFILLTDIRYLAIVAVPALK 138

QY 84 LVTLPFWIHYRGNHMGHGMCKMLSGFYHTGLYSEIFILLTDIRYLAIVAVPALR 143

DB 139 ARTYFGVTVSVITWVAVFASLPGIIFTRSORGLAHT-CSPHFPSQ-YQFKNQTL 196

QY 144 ARTYFGVTVSVITWVAVFASLPGIIFTRSORGLAHT-CSPHFPSQ-YQFKNQTL 201

DB 197 KAVILGLVPLLVAVICSGILTKTLRCRNEKRHRARVLTFTIMYVFLFMAVNYVL 256

QY 202 RMTIFCLVPLLVAVICSGILTKTLRCRNEKRHRARVLTFTIMYVFLFMAVNYVL 260

DB 257 LNTFOEF-FGLNCCSSNRDLQAMQVTELTGTHCCINPIIYAFVGEKFRNYLLVFQKH 315

QY 261 LSSYOSILFG-NDCERSKHLDMVLTVEVIAVSHCCMNPVYAVGFRFRYLRHFRH 319

DB 316 IAKRFCKCSTFOEAPRASSVYTRSTGEDEISV 350

QY 320 LLMHGRYIFLPSEKERTSSV-SPSTAPELSTVF 353

Query Match 54.4%; Score 1502; DB 6; Length 352;

Best Local Similarity 55.2%; Pred. No. 6,19e-208;

Matches 185; Conservative 83; Mismatches 58; Indels 9; Gaps 9;

DB 20 COKINGQIARLLPPLYSLVFVGNILVLLINCKRKSMTDIYLLNLASDLF 79

QY 24 CEKADTRALMAQFVPPLYSLVFVGLGNMNVLLIKYRRLMTNTNYLNLASDLF 83

DB 80 LLTPPEFAHYAAAO-WDEGNTMCOLLGLYFIFGSGIFILLTDIRYLAIVAVPALK 138

QY 84 LVTLPFWIHYRGNHMGHGMCKMLSGFYHTGLYSEIFILLTDIRYLAIVAVPALR 143

DB 139 ARTYFGVTVSVITWVAVFASLPGIIFTRSORGLAHT-CSPHFPSQ-YQFKNQTL 196

QY 144 ARTYFGVTVSVITWVAVFASLPGIIFTRSORGLAHT-CSPHFPSQ-YQFKNQTL 201

DB 197 KAVILGLVPLLVAVICSGILTKTLRCRNEKRHRARVLTFTIMYVFLFMAVNYVL 256

QY 202 RMTIFCLVPLLVAVICSGILTKTLRCRNEKRHRARVLTFTIMYVFLFMAVNYVL 260

DB 257 LNTFOEF-FGLNCCSSNRDLQAMQVTELTGTHCCINPIIYAFVGEKFRNYLLVFQKH 315

QY 261 LSSYOSILFG-NDCERSKHLDMVLTVEVIAVSHCCMNPVYAVGFRFRYLRHFRH 319

DB 316 IAKRFCKCSTFOEAPRASSVYTRSTGEDEISV 350

QY 320 LLMHGRYIFLPSEKERTSSV-SPSTAPELSTVF 353

	Query Match	Score	DB	Length
	Best Local Similarity	54.8%		
		Pred. No. 2,12e-205;		
	Matches	184;	Conservative	84;
			Mismatches	58;
			Indels	9;
			Gaps	9
Db	20	COKINQOIAARLLPPLYSLVFIFEGFVGNIIVLLINCKRIKSKMTDYLLNLTAISDLF	79	
	1-1	1-1	1-1	1-1
Qy	24	CAKPTALMAQFVSLVETVOLLNNVVVYMLIRIRIRITNTYLLNLTAISDLF	83	

RESULT	8	
ID	015538	PRELIMINARY;
AC	015538;	PRT; 352 AA
DT	01-JAN-1998 (TREMIREL, 05, CREATED)	

DB	20	COKINVKQIARLLPPLSLVFI	EGVNMMLVILLINCKRLKSM	TDIYLLNLAISNLF	79
QY <td>24</td> <td>CEKADTRALMAQFVPEPLXSL<td>VFYTGGLGNVVMILLIKYRLR<td>LRMTNLYLNLASDLFF<td>83</td></td></td></td>	24	CEKADTRALMAQFVPEPLXSL <td>VFYTGGLGNVVMILLIKYRLR<td>LRMTNLYLNLASDLFF<td>83</td></td></td>	VFYTGGLGNVVMILLIKYRLR <td>LRMTNLYLNLASDLFF<td>83</td></td>	LRMTNLYLNLASDLFF <td>83</td>	83
Db <td>80</td> <td>LLTVFFMAHYAAQ-WDFGNT</td> <td>MCOLLGLYRIFGFSGIFILLT</td> <td>IDRYLAIVHVAALK</td> <td>138</td>	80	LLTVFFMAHYAAQ-WDFGNT	MCOLLGLYRIFGFSGIFILLT	IDRYLAIVHVAALK	138
QY <td>84</td> <td>LVTLEFWIHYVGHMWFVGHG</td> <td>CKMLSGFYHTGYSSEIFFILL</td> <td>IDRYLAIVHVAFLR</td> <td>143</td>	84	LVTLEFWIHYVGHMWFVGHG	CKMLSGFYHTGYSSEIFFILL	IDRYLAIVHVAFLR	143
Db <td>139</td> <td>ARTVFFGVTVSIMVNVVAF</td> <td>SLDGIITFRQKGLHNTCSH</td> <td>HPYQ-QYFMKNFOTLK</td> <td>197</td>	139	ARTVFFGVTVSIMVNVVAF	SLDGIITFRQKGLHNTCSH	HPYQ-QYFMKNFOTLK	197
QY <td>144</td> <td>ARTVFFGVTVSIMVNGVLA</td> <td>ALPEEIFEYEELEFEETLCS</td> <td>ALPBDYYS-WRHFRTL</td> <td>202</td>	144	ARTVFFGVTVSIMVNGVLA	ALPEEIFEYEELEFEETLCS	ALPBDYYS-WRHFRTL	202
Db <td>198</td> <td>IYILGVLPPLVMVYCSGIL</td> <td>KTLTKCNKRRHRAVLIPTI</td> <td>MYEFLFAPNAYILL</td> <td>257</td>	198	IYILGVLPPLVMVYCSGIL	KTLTKCNKRRHRAVLIPTI	MYEFLFAPNAYILL	257
QY <td>203</td> <td>MTEFLVLPPLVMAICYGII</td> <td>KTLRLCS-KKKKAIPLIIV</td> <td>IAVAFIEMTPYNAIIL</td> <td>261</td>	203	MTEFLVLPPLVMAICYGII	KTLRLCS-KKKKAIPLIIV	IAVAFIEMTPYNAIIL	261
Db <td>258</td> <td>MTFOEF-FGLNNGSSNR</td> <td>LDQAMOVETLGMTGCCIN</td> <td>PIIYAFGEFRNYLLF</td> <td>FOKHI 316</td>	258	MTFOEF-FGLNNGSSNR	LDQAMOVETLGMTGCCIN	PIIYAFGEFRNYLLF	FOKHI 316
QY <td>262</td> <td>SSYQSLILRG-NDCE</td> <td>RSKHLDMVLTVEVIAVS</td> <td>HCQMPVIAFGEPRKYL</td> <td>RNFHRL 320</td>	262	SSYQSLILRG-NDCE	RSKHLDMVLTVEVIAVS	HCQMPVIAFGEPRKYL	RNFHRL 320
Db <td>317</td> <td>AKRFCKCSITQOEPAP</td> <td>ERASSVYTRSGEODIS</td> <td>350</td> <td></td>	317	AKRFCKCSITQOEPAP	ERASSVYTRSGEODIS	350	
QY <td>321</td> <td>LMHLGRYIPFLPSEKLE</td> <td>RTSSV-SPSTAPELISI</td> <td>353</td> <td></td>	321	LMHLGRYIPFLPSEKLE	RTSSV-SPSTAPELISI	353	
RESULT	10				
ID	018772	PRELIMINARY;	PR:	352 AA.	
AC	018772:				
DT	01-JAN-1998	(TREMBLREL. 05, CREATED)			
DT	01-JAN-1998	(TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DT	01-JUN-1998	(TREMBLREL. 06, LAST ANNOTATION UPDATE)			
DE	CCRS RECEPTOR (FRAGMENT).				
GN	CCRS.				
OS	PAN TROGLODITES (CHIMPANZEE).				
OC	EUTARCTA; METAPODA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RA	[1]				
RA	SEQUENCE FROM N. A.				
RC	STRAIN-CHCCRS-142A;				
RA	ZHANG L., CARROthers C. D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,				
RL	HO D. D.;				
RL	AIDS RES. HUM. RETROVIRUSES 0:0-0(1997).				
DR	EMBL; AF011541; G2305200; -.				
DR	PFAM; PF00001: 7tm_1				
FT	NON-TER	352			
SO	SEQUENCE	352 AA; 40598 MW; A9BF8EDF	CRC32;		
	Query Match	53.5%;	Score 1477;	DB 6; Length 352;	
	Best Local Similarity	54.0%;	Pred. No. 5.63e-204;		
	Matches 181; Conservative	87;	Mismatches 58; Indels 9; Gaps 9;		
Db <td>20</td> <td>COKINVKQIARLLPPLSLVFI</td> <td>EGVNMMLVILLINCKRLKSM</td> <td>TDIYLLNLAISDLFF</td> <td>79</td>	20	COKINVKQIARLLPPLSLVFI	EGVNMMLVILLINCKRLKSM	TDIYLLNLAISDLFF	79
QY <td>24</td> <td>CEKADTRALMAQFVPEPLXSL</td> <td>VFYTGGLGNVVMILLIKYRLR</td> <td>LRMTNLYLNLASDLFF</td> <td>83</td>	24	CEKADTRALMAQFVPEPLXSL	VFYTGGLGNVVMILLIKYRLR	LRMTNLYLNLASDLFF	83
Db <td>80</td> <td>LLTVFFMAHYAAQ-WDFGNT</td> <td>MCOLLGLYRIFGFSGIFILLT</td> <td>IDRYLAIVHVAALK</td> <td>138</td>	80	LLTVFFMAHYAAQ-WDFGNT	MCOLLGLYRIFGFSGIFILLT	IDRYLAIVHVAALK	138
QY <td>84</td> <td>LVTLEFWIHYVGHMWFVGHG</td> <td>CKMLSGFYHTGYSSEIFFILL</td> <td>IDRYLAIVHVAFLR</td> <td>143</td>	84	LVTLEFWIHYVGHMWFVGHG	CKMLSGFYHTGYSSEIFFILL	IDRYLAIVHVAFLR	143
Db <td>139</td> <td>ARTVFFGVTVSIMVNVVAF</td> <td>SLDGIITFRQKGLHNTCSH</td> <td>HPYQ-QYFMKNFOTLK</td> <td>197</td>	139	ARTVFFGVTVSIMVNVVAF	SLDGIITFRQKGLHNTCSH	HPYQ-QYFMKNFOTLK	197
QY <td>144</td> <td>ARTVFFGVTVSIMVNGVLA</td> <td>ALPEEIFEYEELEFEETLCS</td> <td>ALPBDYYS-WRHFRTL</td> <td>202</td>	144	ARTVFFGVTVSIMVNGVLA	ALPEEIFEYEELEFEETLCS	ALPBDYYS-WRHFRTL	202
Db <td>197</td> <td>KIVILGVLPPLVMVYCSGIL</td> <td>KTLTKCNKRRHRAVLIPTI</td> <td>MYEFLFAPNAYIYL</td> <td>256</td>	197	KIVILGVLPPLVMVYCSGIL	KTLTKCNKRRHRAVLIPTI	MYEFLFAPNAYIYL	256
QY <td>202</td> <td>RTMIFCLVLPPLVMAICYGII</td> <td>KTLRLCS-KKKYKAIPLI</td> <td>IVIAVAFIEMTPYNAIIL</td> <td>260</td>	202	RTMIFCLVLPPLVMAICYGII	KTLRLCS-KKKYKAIPLI	IVIAVAFIEMTPYNAIIL	260
Db <td>257</td> <td>LNTFOEF-FGLNNGSSNR</td> <td>LDQAMOVETLGMTGCCIN</td> <td>PIIYAFGEKFRNYLL</td> <td>VEFOKH 315</td>	257	LNTFOEF-FGLNNGSSNR	LDQAMOVETLGMTGCCIN	PIIYAFGEKFRNYLL	VEFOKH 315
QY <td>261</td> <td>LSYYSIILRG-NDCE</td> <td>RSKHLDMVLTVEVIAVS</td> <td>HCQMPVIAFGEPRKYL</td> <td>RNFHFRH 319</td>	261	LSYYSIILRG-NDCE	RSKHLDMVLTVEVIAVS	HCQMPVIAFGEPRKYL	RNFHFRH 319
Db <td>316</td> <td>IAKRFCKCSITQOEPAP</td> <td>ERASSVYTRSGEODIS</td> <td>350</td> <td></td>	316	IAKRFCKCSITQOEPAP	ERASSVYTRSGEODIS	350	

 MUSE (TM)

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ch_p protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Dec 8 13:15:36 1998; Maspar time 11.15 Seconds
 854.574 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-963-656-4
 Description: (1-355) from US08963656.pep
 Perfect Score: 2760
 Sequence: 1 MTSLDIVETFGTSTYYDDV.....LERTSSVSPSTAEPLSIVF 355

Scoring table: PAM 150
 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-proc35
 1:swissprot

Statistics: Mean 50.467; Variance 121.099; scale 0.417

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2760	100.0	355	1	CKR3_HUMAN	C-C CHEMOKINE RECEPTOR 0.00e+00
2	2551	92.4	355	1	CKR3_CERAE	C-C CHEMOKINE RECEPTOR 0.00e+00
3	2533	91.8	355	1	CKR3_MACMU	C-C CHEMOKINE RECEPTOR 0.00e+00
4	1960	71.0	359	1	CKR3_MOUSE	PROBABLE C-C CHEMOKINE 0.00e+00
5	1834	66.4	355	1	CKR1_HUMAN	C-C CHEMOKINE RECEPTOR 1.89e-288
6	1723	62.4	355	1	CKR1_MACMU	C-C CHEMOKINE RECEPTOR 6.66e-269
7	1718	62.2	355	1	CKR1_MOUSE	C-C CHEMOKINE RECEPTOR 5.05e-268
8	1507	54.6	352	1	CKR5_CERAE	C-C CHEMOKINE RECEPTOR 1.43e-221
9	1499	54.3	352	1	CKR5_MACMU	C-C CHEMOKINE RECEPTOR 2.14e-228
10	1498	54.3	352	1	CKR5_MOUSE	C-C CHEMOKINE RECEPTOR 2.41e-228
11	1492	54.1	354	1	CKR5_PAPHA	C-C CHEMOKINE RECEPTOR 8.08e-228
12	1489	53.9	352	1	CKR5_GORGO	C-C CHEMOKINE RECEPTOR 1.21e-227
13	1488	53.8	352	1	CKR5_PANTR	C-C CHEMOKINE RECEPTOR 2.71e-227
14	1486	53.8	352	1	CKR5_MOUSE	C-C CHEMOKINE RECEPTOR 6.07e-227
15	1484	53.8	352	1	CKR5_HUMAN	C-C CHEMOKINE RECEPTOR 1.45e-222
16	1459	52.9	373	1	CKR2_MOUSE	C-C CHEMOKINE RECEPTOR 4.57e-219
17	1439	52.1	376	1	CKR2_MOUSE	C-C CHEMOKINE RECEPTOR 6.78e-201
18	1435	48.4	374	1	CKR2_HUMAN	C-C CHEMOKINE RECEPTOR 7.28e-185
19	1243	45.0	360	1	CKR4_HUMAN	C-C CHEMOKINE RECEPTOR 3.26e-177
20	1199	43.4	360	1	CKR4_MOUSE	C-C CHEMOKINE RECEPTOR 2.46e-154
21	1067	38.7	355	1	CKR8_HUMAN	PROBABLE G PROTEIN-COU 5.94e-153
22	1059	38.4	354	1	GPRD_RAT	C-C CHEMOKINE RECEPTOR 1.57e-145
23	1016	36.8	353	1	CKR8_MOUSE	C-C CHEMOKINE RECEPTOR

RESULT	1	ALIGNMENTS
ID	CKR3_HUMAN	STANDARD: PRT: 355 AA.
AC	P51677: Q15748:	
DT	01-OCT-1996 (REL. 34, CREATED)	
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)	
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)	
DE	C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3)	
DE	(EOSINOPHIL EOTAXIN RECEPTOR).	
GN	CKR3	
OS	HOMO SAPIENS (HUMAN)	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;	
OC	EUTHERIA; PRIMATES.	
RP	SEQUENCE FROM N.A.	
RC	TISSUE-MONOCYTES:	
RX	MEDLINE: 95348056	
RA	COMBADIENE C., AHUJA S.K., MURPHY P.M.;	
RL	J. BIOL. CHEM. 270:16491-16494(1995).	
RN	[2]	
RP	ERRATUM.	
RA	COMBADIENE C., AHUJA S.K., MURPHY P.M.;	
RL	J. BIOL. CHEM. 270:30235-30235(1995).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE: 96235044.	
RA	DAUGHERTY B.L., SICILIANO S.J., DEMARTINO J.A., MALKOWITZ L.;	
RL	SIROFINA A., SPRINGER M.S.;	
RN	J. EXP. MED. 183:2349-2354(1996).	
RP	SEQUENCE FROM N.A.	
RA	QIN S., POST T.W., WANG J., WU L., GERARD N.P., NEWMAN W.;	
RL	GERARD C., MACKAY C.R.;	
RN	SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.	
RP	SEQUENCE FROM N.A.	
RA	XIAO L., WEISS S., GARI S., RUDOLPH D., HODGE T., LAL R.;	
RL	SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.	
CC	- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,	
CC	MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY	
CC	INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.	
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.	
CC	- TISSUE SPECIFICITY: IN EOSINOPHILS AS WELL AS TRACE AMOUNTS IN	
CC	NEUTROPHILS AND MONOCYTES.	
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.	
DR	EMBL: U28694; G1199580; -	
DR	EMBL: U51241; G1480481; -	
DR	EMBL: U49727; G1477561; -	

EMBL: AF026535; G2582566; -
DR GCRB; GCR_0988; -
DR GCRB; GCR_1931; -
DR GCRB; GCR_1934; -
DR GCRB; GCR_1993; -
DR GCRB; GCR_2529; -
DR MIM: 601268; -
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 62 1 (POTENTIAL).
FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 93 2 (POTENTIAL).
FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT CONFLICT 276 276 S->T (IN REF. 4).
SQ SEQUENCE 355 AA; 41043 MW; EBI45247 CRC32;

Query Match
Best Local Similarity 100.0%; Score 2760; DB 1; Length 355;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MTSIDVTETFGTSTYDDVGLCEKADTRALMAQFVPLYSIVFTVGLGNVVMILI 60
QY 1 MTSIDVTETFGTSTYDDVGLCEKADTRALMAQFVPLYSIVFTVGLGNVVMILI 60
Db 61 KRRRLRMNINILNLALSDDLFLVLPFWIHVGHNVFSGMKLLSGFHTGLYSE 120
QY 61 KRRRLRMNINILNLALSDDLFLVLPFWIHVGHNVFSGMKLLSGFHTGLYSE 120
Db 121 IFFIILLTDRLAIVHAFALRARTVGTSTYTWGLAVLALPEFIYETEELPEE 180
QY 121 IFFIILLTDRLAIVHAFALRARTVGTSTYTWGLAVLALPEFIYETEELPEE 180
Db 181 TCSAIIYPDIVYSWRHFTLMTIFCLVPLLVMAICYTGIIKTLKCPSSKKRYAIRL 240
QY 181 TCSAIIYPDIVYSWRHFTLMTIFCLVPLLVMAICYTGIIKTLKCPSSKKRYAIRL 240
Db 241 IFVIMAVFIEMTPYVNVALLSYOSILFGNDCESKHLDMVLTVEVIAVSHCCNPIV 300
QY 241 IFVIMAVFIEMTPYVNVALLSYOSILFGNDCESKHLDMVLTVEVIAVSHCCNPIV 300
Db 301 YAFVGERFRKYLRFHFRHMLHGRYIPFLPSEKLERTSSVSPSTAPELCLIVF 355
QY 301 YAFVGERFRKYLRFHFRHMLHGRYIPFLPSEKLERTSSVSPSTAPELCLIVF 355

RESULT 2
ID CKR3_CERAE STANDARD; PRT; 355 AA.
AC P56492;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DE 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3).
GN CMKBR3.
OS CEROPITHECUS AETHIOPS (GREEN MONKEY) (GRIVEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA SOL N., TREBOUET C., GOMAS E., FERCHAL F., ALIZON M.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,

MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: Y13775; E1191907; -
DR GCRB; GCR_2422; -
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 62 1 (POTENTIAL).
FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 93 2 (POTENTIAL).
FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
SQ SEQUENCE 355 AA; 40830 MW; AED65DF8 CRC32;

Query Match
Best Local Similarity 92.4%; Score 2551; DB 1; Length 355;
Matches 327; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

Db 1 MTSIDVTETFGTSTYDDVGLCEKADTRALMAQFVPLYSIVFTVGLGNVVMILI 60
QY 1 MTSIDVTETFGTSTYDDVGLCEKADTRALMAQFVPLYSIVFTVGLGNVVMILI 60
Db 61 KRRRLRMNINILNLALSDDLFLVLPFWIHVGHNVFSGMKLLSGFHTGLYSE 120
QY 61 KRRRLRMNINILNLALSDDLFLVLPFWIHVGHNVFSGMKLLSGFHTGLYSE 120
Db 121 IFFIILLTDRLAIVHAFALRARTVGTSTYTWGLAVLALPEFIYETEELPEE 180
QY 121 IFFIILLTDRLAIVHAFALRARTVGTSTYTWGLAVLALPEFIYETEELPEE 180
Db 181 TCSAIIYPDIVYSWRHFTLMTIFCLVPLLVMAICYTGIIKTLKCPSSKKRYAIRL 240
QY 181 TCSAIIYPDIVYSWRHFTLMTIFCLVPLLVMAICYTGIIKTLKCPSSKKRYAIRL 240
Db 241 IFVIMAVFIEMTPYVNVALLSYOSILFGNDCESKHLDMVLTVEVIAVSHCCNPIV 300
QY 241 IFVIMAVFIEMTPYVNVALLSYOSILFGNDCESKHLDMVLTVEVIAVSHCCNPIV 300
Db 301 YAFVGERFRKYLRFHFRHMLHGRYIPFLPSEKLERTSSVSPSTAPELCLIVF 355
QY 301 YAFVGERFRKYLRFHFRHMLHGRYIPFLPSEKLERTSSVSPSTAPELCLIVF 355

RESULT 3
ID CKR3_MACMU STANDARD; PRT; 355 AA.
AC P56483;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DE 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C CKR-3) (CCR-3).
GN CMKBR3.
OS MACACA MULATTA (RHESUS MACAQUE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA HAUSER D.A., MARGOLIES B.J., CLEMENTS J.E.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA SOL N., TREBOUET C., GOMAS E., FERCHAL F., ALIZON M.;

RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN.
CC MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF017283; G2407219; -
DR EMBL: Y13776; E1192545; -
DR GCRDB: GCR_2424; -
DR GCRDB: GCR_2469; -
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
FT DOMAIN 1 34 1 (POTENTIAL).
FT TRANSMEM 35 62 1 (POTENTIAL).
FT DOMAIN 63 72 2 (POTENTIAL).
FT TRANSMEM 73 93 2 (POTENTIAL).
FT DOMAIN 94 107 3 (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 4 (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 203 5 (POTENTIAL).
FT TRANSMEM 204 223 5 (POTENTIAL).
FT DOMAIN 224 239 6 (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 7 (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 335 7 (POTENTIAL).
FT DISULFID 106 183 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 180 180 K -> E (IN REF. 2).
FT CONFLICT 202 202 K -> R (IN REF. 2).
SO SEQUENCE 355 AA; 40805 MW; A839CACE CRC32;.

Query Match 91.8%; Score 2533; DB 1; Length 355;
Best Local Similarity 91.3%; Pred. No. 0.00e+00;
Matches 324; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

Db 1 MTSLSDFVEFGPTSYDDMGLLCEKADVGALLAOFVPLYSIVFMVGLGNVVMVILI 60
OY 1 MTSLSDFVEFGPTSYDDMGLLCEKADVGALLAOFVPLYSIVFMVGLGNVVMVILI 60
Db 61 KYRRLRIMNTIYLNLALISDLLEFETLPFWIHVYRERNVWFSHOMCKVLSGFEYHGLYSE 120
OY 61 KYRRLRIMNTIYLNLALISDLLEFETLPFWIHVYRERNVWFSHOMCKVLSGFEYHGLYSE 120
Db 121 IFFIILLTDRIYLAIVHAFALRAVTFGVITISVTWGLAVLAALPEFIYEEELFEE 180
OY 121 IFFIILLTDRIYLAIVHAFALRAVTFGVITISVTWGLAVLAALPEFIYEEELFEE 180
Db 181 TLCSAIRPOTVSMRHFHTLKTILCLAPLVMAICVYGIITLRLCPSSKKYKAIRL 240
OY 181 TLCSAIRPOTVSMRHFHTLKTILCLAPLVMAICVYGIITLRLCPSSKKYKAIRL 240
Db 241 IFTVMAVEFIFMPPYNAIISTVQSIVLFGDCEKSHLDLFEVLADEVIAVSHCCVAPVI 300
OY 241 IFTVMAVEFIFMPPYNAIISTVQSIVLFGDCEKSHLDLFEVLADEVIAVSHCCVAPVI 300
Db 301 YAFVGEFRKRYLRHFRRHVLMLGKXIPPLSEKLETSVSPSTAEPLISIVF 355
OY 301 YAFVGEFRKRYLRHFRRHVLMLGKXIPPLSEKLETSVSPSTAEPLISIVF 355

RESULT 4
ID CRR3_MOUSE STANDARD; PRT; 359 AA.
AC P51678;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PROBABLE C-C CHEMOKINE RECEPTOR TYPE 3 (C-C-CRR-3) (CC-CRR-3) (CCR-3)
DE (MACROPHAGE INFLAMMATORY PROTEIN-1 ALPHA RECEPTOR-LIKE 2) (MIP-1 ALPHA
DE R12).
DE CCKBR3 OR CCKBR1L2.
OS MRS MUSCULUS (MOUSE).
OS EUKARIOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-129/SV;
RX MEDLINE: 96072806.
RA POST T.M., BOZIC C.R., ROTHENBERG M.E., LUSTER A.D., GERARD N.,
RA GERARD C.;
RA J. IMMUNOL. 155:5299-5305(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-129/SV;
RX MEDLINE: 95340546.
RA GAO J.-L., MURPHY P.M.;
RA J. BIOL. CHEM. 270:17494-17501(1995).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,
CC MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: DETECTED IN SKELETAL MUSCLE AND IN TRACE
CC AMOUNTS IN LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: U29677; G1109784; -
DR EMBL: U28406; G1203801; -
DR GCRDB: GCR_1673; -
DR GCRDB: GCR_1695; -
DR MGD: MGI:104616; CCKBR1L2.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
FT DOMAIN 1 38 1 (POTENTIAL).
FT TRANSMEM 39 64 1 (POTENTIAL).
FT DOMAIN 65 68 2 (POTENTIAL).
FT TRANSMEM 69 95 2 (POTENTIAL).
FT DOMAIN 96 111 3 (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 150 4 (POTENTIAL).
FT TRANSMEM 151 175 4 (POTENTIAL).
FT DOMAIN 176 201 5 (POTENTIAL).
FT TRANSMEM 202 227 5 (POTENTIAL).
FT DOMAIN 228 243 6 (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 7 (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 359 7 (POTENTIAL).
FT DISULFID 110 187 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 270 270 R -> S (IN REF. 2).
SO SEQUENCE 359 AA; 41825 MW; 3D2A9F0D CRC32;.

Query Match 71.0%; Score 1960; DB 1; Length 359;
Best Local Similarity 70.5%; Pred. No. 0.00e+00;
Matches 246; Conservative 51; Mismatches 50; Indels 2; Gaps 2;

Db 12 VESFEPTPEYEWAPP-CEVRIKELGSWLPPLYSIVFLIGLMMVMVILIYKRIQ 70
OY 8 VEFEGTTSY-YDVGGLCEKADTRALMAOFVPLYSIVFLVGLGNVVMVILIYKRIQ 66
Db 71 IMNTIYLNLALISDLLEFETLPFWIHVYVLMNENGFHGMCKMLSGFYALAYSEIFIIIL 130
OY 67 IMNTIYLNLALISDLLEFETLPFWIHVYRGNHNVFSGHGMCKMLSGFYHGLYSEIFIIIL 126
Db 131 LITDRIYLAIVHAFALRAVTFATITSTITWGLAGLALPEFIHESODSFEESQSPR 190
OY 127 LITDRIYLAIVHAFALRAVTFGVITISVTWGLAVLAALPEFIYEEELFEEELCSAL 186
Db 191 YPEGEEDSKRFHRLRNINIGLAPLLVNYICSGIITKTLRCPNKKHKAIRLIFVMI 250
OY 187 YPEDITYSMRHFHTLKTILCLAPLVMAICVYGIITLRLCPSSKKYKAIRLIFVIMA 246
Db 251 VEFIFMTPLVLLFSAFHTPLETSCEDSKHLDLMAQVTEVLAAYTHCCVNPYAVGGE 310
OY 247 VEFIFMTPLVNAIISTVQSIVLFGDCEKSHLDLVMALVTEVIAVSHCCVNPYAVGGE 306
Db 311 RFKKHLRHFRRHVNAYVYLGKIFPLFGKKMERKTSVSPSTGEDEISIVF 359
OY 311 RFKKHLRHFRRHVNAYVYLGKIFPLFGKKMERKTSVSPSTGEDEISIVF 359

Query Match 62.4% Score 1723; DB 1; Length 355;
Best Local Similarity 60.1% Pred. No. 6.66e-269;
Matches 215; Conservative 69; Mismatches 68; Indels 6; Gaps 6;

DB 1 METP-MTTEDDYDITFEEDGADATP-CHKVERAIIAQLPPLSLVFIQVGNLVILV 58
1 MTSLSDTVEFG-TTSTV-YDVGLLCEKADTRALMAQFVPLSLVFTVGLGNVYVMTL 58
OY 1 MTSLSDTVEFG-TTSTV-YDVGLLCEKADTRALMAQFVPLSLVFTVGLGNVYVMTL 58
DB 59 LVOYKRLKMTNTIYLLNLALISDLLEFTLPFLIYKSTDMIFGDACKLLSGFYTG 118
OY 59 LKRYRLRMTNTIYLLNLALISDLLEFTLPFLIYKSTDMIFGDACKLLSGFYTG 118
DB 119 SEIFFIILLIDRYLAIVHAFVFLARVTFGYTSTIIIMALLASSPLMTFSKOWNI 178
OY 119 SEIFFIILLIDRYLAIVHAFVFLARVTFGYTSTIIIMALLASSPLMTFSKOWNI 178
DB 179 VRHS-CNHFPEYSPQOQKLFQALKNLFGVLPLVLMVICYGIIKILRRPNEKSK 237
OY 178 FEETLSALYEDTVYSWRHFTLRMTIFGLVPLVLMACIYGIITKLRCPSKKRYA 237
DB 238 VRLIYIMIFELFWTPYNLTLSVFOEFLTHLCEQNDLAMEVTEVIANMHCVN 297
OY 238 IRLIYIMAFEFIFMTYPYNAIILSSYOSILFGNDCERSKHLDMVTEVIAVSHCMN 297
DB 298 PVIYAAGEFRKYLQLFHRRVAVHVKLPFLSGDRLEAVSTSPSGEHLGAGF 355
OY 298 PVIYAAGEFRKYLQLFHRRVAVHVKLPFLSGDRLEAVSTSPSGEHLGAGF 355

RESULT 7
ID CKRLMOUSE STANDARD; PRT; 355 AA.
AC P51675;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-C CHEMOKINE RECEPTOR TYPE 1 (C-C CKR-1) (CCR-1)
DE (MACROPHAGE INFLAMMATORY PROTEIN-1 ALPHA RECEPTOR) (MIP-1ALPHA-R)
DE (RANTES-R).
GN CMKBR1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-129/SV; TISSUE-PERITONEAL MACROPHAGE;
RA MEDLINE: 96072806.
RA POST T.W., BOZIC C.R., ROTHENBERG M.E., LUSTER A.D., GERARD N.,
RA GERARD C.;
RA J. IMMUNOL. 155:5299-5305(1995).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN-129/SV;
RX MEDLINE: 95340546.
RA GAO J.-L., MURPHY P.M.;
RA J. BIOL. CHEM. 270:17494-17501(1995).
RL J. BIOL. CHEM. 270:17494-17501(1995).
CC -I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1 ALPHA,
CC RANTES, AND LESS EFFICIENTLY, TO MIP-1 BETA OR MCP-1 AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
CC PROLIFERATION.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: DETECTED IN THE HEART, SPLEEN, LUNG,
CC PERITONEAL EXUDATE CELLS AND LEUKOCYTES.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: U29678; G1109786;
DR EMBL: U28404; G881548;
DR GCRDB: GCR_1672;
DR GCRDB: GCR_1696;
DR MGD: MGI:104618; CMKBR1.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
KM G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
RN

FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 6 (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 7 (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 7 (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT CONFLICT 55 55 M -> V (IN REF. 2).
SQ SEQUENCE 355 AA; 40901 MW; A842B9D8 CRC32;

Query Match 62.2% Score 1718; DB 1; Length 355;
Best Local Similarity 58.1% Pred. No. 5.05e-268;
Matches 207; Conservative 83; Mismatches 64; Indels 2; Gaps 2;

DB 1 MEIS-DFTBAYPTTPEFDYDSTPCOKTAVRAFGALPPLSLVFIQVGNLVILV 59
OY 1 MTSLSDTVEFTGTSYD-DVGLCEKADTRALMAQFVPLSLVFTVGLGNVYVMTL 59
DB 60 MOHRLQSMSTIYLFENLAVSDLVLEFLFPWIDYKLDKDMIFGDACKLLSGFYTG 119
OY 60 IKYRLRMTNTIYLLNLALISDLLEFTLPFLIYKSTDMIFGDACKLLSGFYTG 119
DB 120 EIFFIILLIDRYLAIVHAFVFLARVTFGYTSTIIIMALLASSPLMTFSKOWNI 179
OY 120 EIFFIILLIDRYLAIVHAFVFLARVTFGYTSTIIIMALLASSPLMTFSKOWNI 179
DB 180 HRTSPHFPYKSLKQMRQALKNLGLPLVLIYCYAGIIRILRRPSEKRYAVR 239
OY 180 EITLSALYEDTVYSWRHFTLRMTIFGLVPLVLMACIYGIITKLRCPSKKRYA 239
DB 240 LIFAITLFLPMTYPLNLSVFAFODVLTNQCQSKHLDLAMOYTEVIAVTHCCVNP 299
OY 240 LIFVIMAVFEFMTYPYNAIILSSYOSILFGNDCERSKHLDMVTEVIAVSHCMN 299
DB 300 IYAFVGEFRKYLQLFHRRVAVHVKLPFLSGDRLEAVSTSPSGEHLGAGF 355
OY 300 IYAFVGEFRKYLQLFHRRVAVHVKLPFLSGDRLEAVSTSPSGEHLGAGF 355

RESULT 8
ID CKR5_MACMU STANDARD; PRT; 352 AA.
AC P79436; 002746;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CMKBR5.
OS MACACA MUTATTA (RHESUS MACAQUE), MACACA FASCICULARIS (CRAB EATING
OS MACAQUE) (CYNOMOLGUS MONKEY), AND MACACA NEMESTRINA (PIG-TAILED
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RN SEQUENCE FROM N.A.
RP SPECIES-M. MUTATTA;
RX MEDLINE: 97184592.
RA MARCON L., CHOE H., MARTIN K.A., FARZAN M., POUATH P.D., WU L.,
RA NEWMAN W., GERARD N., GERARD C., SODROSKI J.;
RA J. VIROL. 71:2522-2527(1997).
RN [2]
RN SEQUENCE FROM N.A.
RP SPECIES-M. MUTATTA; STRAIN-INDIAN MACAQUE;
RX MEDLINE: 97213934.
RA CHEN Z., ZHOU P., HO D.D., LANDAU N.R., MARX P.A.;
RA J. VIROL. 71:2703-2714(1997).
RN [3]

RP SEQUENCE FROM N.A.
RC SPECIES=M.MULATTA.
RA HAUBER D.A., MARGOLIS B.J., CLEMENTS J.E.,
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
[4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.MULATTA. M.FASCICULARIS AND M.NEMESTRINA;
RA EDINGER A.L., AMEDEE A., MILLER K., DORANZ B.J., ENDRES M.,
RA SHARON M., SAMSON M., LU Z.H., CLEMENTS J.E., MURPHEY-CORB M.,
RA PEIDER S.C., PARMENTIER M., BRODER C.C., DONS R.W.;
RL PROC. NATL. ACAD. SCI. U.S.A. 94:4005-4010(1997).
CC -I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: U77672; G1850350; -;
DR EMBL: U77379; G1771981; -;
DR EMBL: U96762; G2088633; -;
DR EMBL: AF005660; G2245614; -;
DR EMBL: AF005661; G2245616; -;
DR EMBL: AF005662; G2245618; -;
DR GCRDB: GCR_1286; -;
DR GCRDB: GCR_1369; -;
DR GCRDB: GCR_1370; -;
DR GCRDB: GCR_1371; -;
DR GCRDB: GCR_1639; -;
DR GCRDB: GCR_1641; -;
DR PROSITE: PS00237; G-PROTEIN RECEPTOR. 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT TRANSMEM 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT CARBOHYD 268 268
FT CONFLICT 241 241
FT CONFLICT 292 292
SQ SEQUENCE 352 AA; 40507 MW; 9E6826EC CRC32;
Query Match 54.6%; Score 1507; DB 1; Length 352;
Best Local Similarity 55.5%; Pred. No. 5,67e-231;
Matches 186; Conservative 83; Mismatches 57; Indels 9; Gaps 9;

DB 257 INTFOEF-FGLNCCSSNRDLQAMQVTELTGMCNCPITPIYAFGEKFRNVLVFEOKH 315
OY 261 LSSYSILFG-NDCCRSKHLDMVLVEVIAVSHCCNMPVIAAFGEFRRLRHFRRH 319
DB 316 IAKRCKCSIFQCAPRASSVYRSGEOEISV 350
OY 320 LLMHLGRYIPFLPSKERTSSV-SPSTAPELST 353
RESULT 9
ID CKR5 CERAE STANDARD: PRT: 352 AA.
AC P56493; 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DR 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
GN CKR5
OS CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUHERIA; PRIMATES.
RP [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE: 98001387.
RA KUHMANN S.E., PLATT E.J., KOZAK S.L., KABAT D.;
RL J. VIROL. 71:8642-8656(1997).
CC -I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: U83324; G2347108; -;
DR EMBL: U83325; G2347110; -;
DR GCRDB: GCR_2465; -;
DR GCRDB: GCR_2466; -;
DR PROSITE: PS00237; G-PROTEIN RECEPTOR. 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; POLYMORPHISM.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT VARIANT 14 14
FT VARIANT 352 352
SQ SEQUENCE 352 AA; 40561 MW; 9CA7E235 CRC32;
Query Match 54.3%; Score 1499; DB 1; Length 352;
Best Local Similarity 55.2%; Pred. No. 1.43e-229;
Matches 186; Conservative 83; Mismatches 59; Indels 9; Gaps 9;

	Best Local Similarity	55.28;	Pred. No.	2,14e-229;	Mismatches	185;	Conservative	57;	Indels	9;	Gaps	
Db	20	COKINVKQIARBLRPLSVLFIIFGFGVGNILVVLLINCKRKLSMTDIYLLNLAISDLF	79									
Qy	24	CEKADRTALMAQGVPLPSLVFTVGGLGNVVMYLIKRRLIRIMNTIYLLNLAIISDLF	83									
Db	80	LIIYVFPAHIAAAAO-WDFGNTMCOILLTGLTFIFSESGIFPIILLTDRLAIVAHAVALK	138									
Qy	84	LVTLPEVIHYVRHHNNWFFGHGMCKLLSGFHNGLYSEIFFIILLTDRLAIVAHAVFALR	143									
Db	139	ARYTEPVMVSLTMVAVVASLPGLIIFFRSOREGHLHV-CSSHFPYSQ-YQFMKNFOFL	196									
Qy	144	ARYTEPVITISVTWGVALVAAPLEEIFETE-ELEEETLSALHPEDTVYS-WRFPHVL	201									
Db	197	KIVILGLVLPDLNVVICSYSGILTKLLRCNRKKRRHRAVLIIFIMIVYLFMAPYIVVL	256									
Qy	202	RMTIFCVLPDLVLMALICYSTIIKTLLRCP-KKKYKAINDIPIAMVFEIPMPYVAL	260									
Db	257	LNTFQEF-FELANCCSSNRILDQAOMVETLGMTGCCINPIIYAEGEKFNRYLLVFFQRH	315									
Qy	261	LSVSOSILFG-NDCERSKHLDLVMALTVEVIAVSAHCMPPIYAFVGERPRKYLRHFHRH	319									
Db	316	IARFCCKCSIFQDEAPERASSYTSTGEQLSV	350									
Qy	320	LMHLGRYIPLFEPSEKLERTSSV-SPTAPELISI	353									
RESULT	11	STANDARD:	PRT:	354 AA.								
ID	CKRS_RAT											
AC	O08536;											
DT	01-NOV-1997 (REL. 35, CREATED)											
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)											
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)											
DE	C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CCR-5) (CCR-5) (MIP-1 ALPHA RECEPTOR).											
GN	CMKBRS.											
OS	RATTUS NORVEGICUS (RAT).											
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPLATA; MAMMALIA;											
OC	EUTHERIA; RODENTIA.											
RN	[1]											
RP	SEQUENCE FROM N.A.											
RC	STRAIN=WISTAR; TISSUE=BRAIN;											
RA	SLETISLS O., GORMALA N., BODDERE H.W.G.M., SAUER A., BERGER M.,											
RA	GEBIKE-HARTER P.J.;											
RL	SUBMITTED (MAR-1997). TO EMBL/GENBANK/DDJ DATA BANKS.											
CC	-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1 ALPHA											
CC	MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY											
CC	INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.											
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.											
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.											
DR	EMBL: Y12009; E309267; ..											
DR	GGDB: GCR_1470; -											
DR	PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.											
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.											
FT	DOMAIN	1	32									
FT	TRANSMEM	33	60									
FT	DOMAIN	61	70									
FT	TRANSMEM	71	91									
FT	DOMAIN	92	104									
FT	TRANSMEM	105	126									
FT	DOMAIN	127	143									
FT	TRANSMEM	144	168									
FT	DOMAIN	169	200									
FT	TRANSMEM	201	220									
FT	DOMAIN	221	237									
FT	TRANSMEM	238	262									

RA DORANZ B.J., LU Z.H., RUCKER J., ZHANG T.Y., SHARRON M., CEN Y.H.,
 RA WANG Z.X., GUO H.H., DU J.G., ACCAVITTI M.A., DOMS R.W., PEIPER S.C.,
 RL J. VIROL. 71:6305-6314(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA GUO B., KUNO K., HARADA A., MATSUSHIMA K.,
 RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
 CC BUT NOT IN NONHEMATOPOIETIC CELL LINES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: U47036; G1237136; -
 DR EMBL: X94151; E218395; -
 DR EMBL: U68565; G1698716; -
 DR EMBL: U83327; G2347114; -
 DR EMBL: AF022990; G2444487; -
 DR EMBL: AF019772; G2431976; -
 DR EMBL: D83648; G1777330; -
 DR GCRDB: GCR_1150; -
 DR GCRDB: GCR_1645; -
 DR GCRDB: GCR_1656; -
 DR GCRDB: GCR_1729; -
 DR GCRDB: GCR_2448; -
 DR GCRDB: GCR_2540; -
 DR GCRDB: GCR_2554; -
 DR MGD: MGI:107182; CMKR5.
 DR PROSITE: PS00237; G-PROTEIN RECEPTOR; 1.
 DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; POLYMORPHISM.
 KM DOMAIN 1 32
 FT TRANSMEM 33 60
 FT DOMAIN 61 70
 FT TRANSMEM 71 91
 FT DOMAIN 92 104
 FT TRANSMEM 105 126
 FT TRANSMEM 127 143
 FT TRANSMEM 144 168
 FT DOMAIN 169 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 237
 FT TRANSMEM 238 262
 FT TRANSMEM 263 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 354
 FT DISULFID 103 180
 FT CARBOHYD 270 270
 FT VARIANT 11 11
 FT VARIANT 62 62
 FT VARIANT 66 66
 FT VARIANT 97 97
 FT VARIANT 109 109
 FT VARIANT 156 156
 FT VARIANT 160 160
 FT VARIANT 185 185
 FT VARIANT 213 213
 FT VARIANT 318 318
 FT VARIANT 337 337
 FT VARIANT 3 3
 FT CONFLICT 80 80
 FT CONFLICT 190 190
 FT CONFLICT 208 208
 FT CONFLICT 145 145
 SO SEQUENCE 354 AA; 40863 MW; 6ECD306A CRC32;
 Query Match 53.98; Score 1488; DB 1; Length 354;
 Best Local Similarity 54.48; Pred. No. 1.21e-227;
 Matches 181; Conservative 82; Mismatches 63; Indels 7; Gaps 7;
 Db 22 COKINVAQIAQLPLPVSVIFGFGVNMVFLILSKCKLKSVFQIYLLNLATISDLF 81
 Oy 24 CERKDTBALMAQFVPLPLXSLVFTYGLGNVYVAILIKRYRLRINTIYLLNLATISDLF 83

Db 82 LTLPLPMANHA-ANEMIFGNCKVETGYVHIGEGCIPFIILLITDRYLAIVHAFALK 140
 Oy 84 LVLPFWIHVYRGHNMVFGHCKLLSGFYHTGLYSEIFILLITDRYLAIVHAFALR 143
 Db 141 VRTVNGVITSVTVWVAVASAPLEIIFTRSKQEGHYT-CSPHPFTHQVHFKSQTOK 199
 Oy 144 ARVTVGVITSITWGLAVIALPEFIYETE-ELEBEITCSLLYEDVYSRHHHTLR 202
 Db 200 MVLISLPLLVMIICYSGLIATLFCRNEKRRHRAVRLFAIMYVFLFMPYNIYVLL 259
 Oy 203 MTFICVLPLVLAICVGTGKITLLKOPS-KKKYKAIRLFVIMAVFIIWTFYVNAILL 261
 Db 260 TTRQEF-FGLNCCSSNRDLQAMQATETLGMHCCNPVYAVGEKRSYSVFERKHI 318
 Oy 262 SSYOSILF-NDCKRSKHDLVMLVTEVIAVSHCCNMPYVAVGERFRKYLHFFHRL 320
 Db 319 VKRFCKRSIFQDNDPDRVSVYTRSTGEHVS 351
 Oy 321 LMHLGRITPLPSEKLERTSSV-SPSTAPELS 352
 RESULT 14
 ID PK6440; 002778; PRT; 352 AA.
 AC 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
 GN CMKR5.
 OS PAN TROGLODYTES (CHIMPANZEE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97268687.
 RA EDINGER A.L., AMEDEE A., MILLER K., DORANZ B.J., ENDRES M.,
 RA SHARRON M., SANSON M., LU Z.H., CLEMENTS J.E., MURPHEY-CORB M.,
 RA PEIPER S.C., PARMENTER M., BRODER C.C., DOMS R.W.,
 RA PROC. NATL. ACAD. SCI. U.S.A. 94:4005-4010(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA ZIMMERMAN P.A., BOCKLER-WHITE A., ALKHATTI G.,
 RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98022612.
 RA ZHANG L., CARROTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
 RA HO D.D.,
 RL AIDS RES. HUM. RETROVIRUSES 13:1357-1366(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97426118.
 RA ZACHAROVA V., ZACHAR V., GOSTIN A.S.,
 RL AIDS RES. HUM. RETROVIRUSES 13:1159-1161(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98090115.
 RA PRETET J.-L., ZERBIB A., GIRARD M., GUILLET J.-G., BUTOR C.,
 RL AIDS RES. HUM. RETROVIRUSES 13:1583-1587(1997).
 CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
 CC DIFFERENTIATION.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF005663; G245620; -
 DR EMBL: U94329; G2145188; -
 DR EMBL: AF011542; G2305202; -
 DR EMBL: U97666; G2327059; -
 DR EMBL: AF011540; G2305198; -
 DR EMBL: U89797; G2281445; -

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DR GCRDB: GCR_1284;
DR GCRDB: GCR_1357;
DR GCRDB: GCR_2432;
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 51 58 1 (POTENTIAL).
FT DOMAIN 59 68 1 (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT CARBOHYD 268 268 POTENTIAL.
FT CONFLICT 123 123 T -> S (IN REF. 1).
SEQUENCE 352 AA; 40539 MW; D6554684 CRC32;

Query Match 53.8%; Score 1486; DB 1; Length 352;
Best Local Similarity 54.6%; Pred. No. 2, 71e-227;
Matches 183; Conservative 86; Mismatches 57; Indels 9; Gaps 9;

DB 20 CCKINVKQIAALLPLPLYSVLFPGVGMVILILINCKRILKSMIDILNLATISDFE 79
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 24 CKAQDRAIMAFVPLPLSLVFTVGLGNVVVMILIKRIRIMINITYILNLATISDLF 83
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 80 LITVEFWAHYAAQ-WDEGNTMCOILTGFLTGFSSGIFILLIDRYLAIVHAFALK 138
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 84 LVTLPFWIHVGHMNVFCHGMCKILSGFYHGLYSEIFILLIDRYLAIVHAFALK 143
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 139 AATVTFGVATVITVNVAVFASLPGIIFTRSQEGLHT-CSSHFYSO-YQEMKNFQL 196
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 144 AATVTFGVATVITVNVAVFASLPGIIFTRSQEGLHT-CSSHFYSO-YQEMKNFQL 201
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 197 KVIIVGLVPLVWVYCYSGILKTLRCNKKRHRVLFITIMVYFLFAPRYIVL 256
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 202 KATICLVPLVMAICYIITKILRCS-KKRYAHLIYIVAVFIEFPIVAVL 260
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 257 LNTFOEF-FGLNCSNNLDQAMOVETLGMTHCCINPIIYAVGEKRNVLVFFQKH 315
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 261 LSSYSILFG-NDCEKSKHLDMVLTETVYAVSHCCMNVYIAFVGERRKYLRHFHRH 319
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 316 IAKRCKCSIFQEPAPERASSVYITSGEOELSV 350
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 320 LLMHGRYIPFLPSEKERTSSV-SPSTAEPELSI 353
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
ID CCR5_HUMAN STANDARD. PRI: 352 AA.
AC PS1881; 014692; 014693; 014695; 014696; 014697; 014698; 014699;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE C-C CHEMOKINE RECEPTOR TYPE 5 (C-C CCR-5) (CC-CCR-5) (CCR-5) (CCR5)
DE (HIV-1 FUSION CO-RECEPTOR) (CHEMR13).
GN CCR5.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96241590.
RA SAMSON M., LABBE O., MOLLEREAU C., VASART G., PARMENTIER M.,
RL BIOCHEMISTRY 35:3362-3367(1996).
RN [2]
RP SEQUENCE FROM N.A.

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RX MEDLINE: 96291862.
RA RAPORT C.J., GOSLING J., SCHWEICHAUT V.L., GRAY P.W., CHARO I.F.;
RA J. BIOL. CHEM. 271:17161-17166(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96295970.
RA COMBADIERE C., ANJUA S.K., TIEFANY H.L., MURPHY P.M.;
RA J. LEUKOC. BIOL. 60:147-152(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA MCCOMBIE W.R., WILLSON R., CHEN E., GIBBS R., ZUO L., JOHNSON D.,
RA NHAN M., PARMENTIER L., DEHIA N., ANSARI A., MARDIS E., SCHUTZ K.,
RA GNOJ L., LA BASTIDE M., KAPLAN N., GRECO T., TOUCHMAN J.,
RA MUZY D., CHEN C.N., EVANS C., FITZGERAID M., SEE L.H., TANG M.,
RA PORCEL B.M., DRAGAN Y., GIACALONE J., PAE A., POWELL E.,
RA SOLINSKY K.A., DESILVA U., DIAZ-PEREZ S., ZHOU X., YU Y.,
RA WATANABE M., DOGGETT N., GARCIA D., SAGRIPANTI J.L.;
RA SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDJ DATA BANKS.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98001387.
RA KUHMANN S.E., PLATT E.J., KOZAK S.L., KABAT D.;
RA J. VIROL. 71:8642-8656(1997).
RN [6]
RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX MEDLINE: 98022612.
RA ZHANG L., CARUTHERS C.D., HE T., HUANG Y., CAO Y., WANG G., HAHN B.,
RA HO D.D.;
RA AIDS RES. HUM. RETROVIRUSES 13:1357-1366(1997).
RN [7]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE: 96260017.
RA DENG H., LIU R., ELMETIER W., CHOE S., UNUTMAZ D., BURKHART M.,
RA DI MARZO P.C., MARMON S., SUTTON R.E., HILL C.M., DAVIS C.B.,
RA PEPPER S.C., SCHALL T.J., LITTMAN D.R., LANDAU N.R.;
RA NATURE 381:661-666(1996).
RN [8]
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
RX MEDLINE: 96260018.
RA DRAGIC T., LITWIN V., ALLAWAY G.P., MARTIN S.R., HUANG Y.,
RA NAGASHIMA K.A., CAVANAN C., MADDON P.J., KOUP R.A., MOORE J.P.,
RA PAYTON W.A.;
RA NATURE 381:667-673(1996).
RN [9]
RP FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -I- FUNCTION: ACTS AS CO-RECEPTOR WITH CD4 FOR PRIMARY NON-
CC SYNCYTUM-INDUCING STRAINS (NSI) (MACROPHAGE-TROPIC) OF HIV-1
CC VIRUS. IT PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: FOUND IN PROMYELOCYTIC CELLS.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
DR EMBL: X9192; E199247; -
DR EMBL: U54994; G1457946; -
DR EMBL: U57840; G1502409; -
DR EMBL: U95626; G2104520; -
DR EMBL: U83326; G2347112; -
DR EMBL: AF011500; G2305118; -
DR EMBL: AF011501; G2305120; -
DR EMBL: AF011502; G2305122; -
DR EMBL: AF011503; G2305124; -
DR EMBL: AF011505; G2305128; -
DR EMBL: AF011506; G2305130; -
DR EMBL: AF011507; G2305132; -
DR EMBL: AF011508; G2305134; -
DR EMBL: AF011509; G2305136; -
DR EMBL: AF011510; G2305138; -
DR EMBL: AF011511; G2305140; -
DR EMBL: AF011512; G2305142; -
DR EMBL: AF011513; G2305144; -
DR EMBL: AF011514; G2305146; -

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Best Local Similarity 54.3%; Pred. No. 6,07e-227;
Matches 182; Conservative 87; Mismatches 57; Indels 9; Gaps 9

Dd      20 COKINVKOIAARLLPPLTSLVIFGFVGNMVLVILINICKRLKSMTDLYLNLAIISDLFF 79
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      24 CEKADTRALMAQFNPPLXSLVFTYGLGAGVYVYVAILIKRYRLRIMTNTYLNLAISDLFF 83
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Dd      80 LLYVPEFMAHYAAQ-WDEGNTMCOLLTGLGYEIGFSSGIFILLTIDRYLAVHVAFAK 138
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      84 LYLTEFHWIHYVRGNHWVGHGMCKLLSGEYHTGLYSEFFILLTIDRYLAVHVAFAK 143
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Dd      139 ARTVTEFGVTVYITWVAVFASLPGIIFTRQKQEGHLYT-CSSHPYPSQ-YQFKNFQTL 196
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      144 ARTVTEFGVTVISVTMGLVLAALPEFIFYETE-ELFETELTSAIYAPEDTVYS-WRHFHTL 201
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Dd      197 KIVILGVLPLPLVWVYICSGILKTLTLNRGNKKRHRARLFTLTIMVYELFMAPRYNIVL 256
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      202 RMTTFICVLPLPLVMAICTGITLIKTLRLKPS-KKKYKARLLFVMAVFIWITWYNAVL 260
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :






Dd      257 INTPEOF-FGLINCCSSNRLDQAAQVTELTGMCACINPIIYAEVGEKFRNYLLVFQKH 315
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      261 LSSYQSLIFG-NDCRSKSHDLVNLVTELVIAVSHCCMNPVIYARVGEFRKYLHFFHRH 319
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Dd      316 IAKRFCKCCCSIFQOEAPERASSVYTRSTGEODEISV 350
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      320 LLMHLGRYIPFLPSEKLETERTSSV-SPSTAPELSTI 353
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: Tue Dec 8 13:16:05 1998
Job time : 29 secs.

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ENTRY      A57237      #type complete
TITLE      Chemokine (C-C) receptor 3 - human
ALTERNATE_NAMES C-C CKR-3
ORGANISM   Homo sapiens #common_name man
DATE       08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change
          29-Aug-1997
ACCESSIONS A57237
REFERENCE   A57237
#authors   Combiadere, C.; Ahuja, S.K.; Murphy, P.M.
#journal   J. Biol. Chem. (1995) 270:16491-16494
#title     Cloning and functional expression of a human eosinophil CC
           chemokine receptor.
#accession A57237
#status    preliminary; nucleic acid sequence not shown
#molecule-type mRNA
#residues  1-355 #label CCM
#cross-references GB:U28694

GENETICS
#gene      GDB:CMKBR3
#cross-references GDB:579624; CMIM:601268
#map_position 3p21-3p21
#WORDS     6 protein-coupled receptor; glycoprotein; phosphoprotein;
           transmembrane protein
#FEATURES
36-60      #domain transmembrane #status predicted #label TM1\
71-91      #domain transmembrane #status predicted #label TM2\
108-129    #domain transmembrane #status predicted #label TM3\
147-171    #domain transmembrane #status predicted #label TM4\
205-223    #domain transmembrane #status predicted #label TM5\
240-261    #domain transmembrane #status predicted #label TM6\
288-305    #domain transmembrane #status predicted #label TM7\
24-273,106-183
           #disulfide bonds #status predicted\
           #binding-site phosphate (Ser) (covalent) (by casein
           kinase II) #status predicted
SUMMARY    #length 355 #molecular-weight 41072 #checksum 897

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Best Local Similarity 99.4%; Pred. No. 0.00e+00;
Matches 353; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MTSLSDTVEFTGTSYDDVGLCEKADTRALMAQFVPPLSLVFTVGLGNVVMILI 60
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QY 1 MTSLSDTVEFTGTSYDDVGLCEKADTRALMAQFVPPLSLVFTVGLGNVVMILI 60

Db 61 KRRRLRIMNIIYLNLAIISDLFLVLPFWIHVYRGHNWFGHGMCLISGFYHGLYSE 120
    |||||
QY 61 KRRRLRIMNIIYLNLAIISDLFLVLPFWIHVYRGHNWFGHGMCLISGFYHGLYSE 120

Db 121 IFFIILLTDRYLAIVHAFALRARTVFGVITSIYTWGLAVLAALPEFIYETEELFEE 180
    |||||
QY 121 IFFIILLTDRYLAIVHAFALRARTVFGVITSIYTWGLAVLAALPEFIYETEELFEE 180

Db 181 TICSALYPEDTVYSWRHFTLRMTIFCLVPLVMAICYGILIKLRPSKKKYAIRL 240
    |||||
QY 181 TICSALYPEDTVYSWRHFTLRMTIFCLVPLVMAICYGILIKLRPSKKKYAIRL 240

Db 241 IFYIMAVFIFMTPIYVAILLSYQSILFGNDCERSKHLDRVWLVTETVAYSHCCNPVI 300
    |||||
QY 241 IFYIMAVFIFMTPIYVAILLSYQSILFGNDCERSKHLDRVWLVTETVAYSHCCNPVI 300

Db 301 YAFVGRFRKRYLRHFFRHLMLHGRYIPFLPSEKLERTSSVSPSTAEPLSLVF 355
    |||||
QY 301 YAFVGRFRKRYLRHFFRHLMLHGRYIPFLPSEKLERTSSVSPSTAEPLSLVF 355

RESULT      3
ENTRY      149341      #type complete
TITLE      MIP-1 alpha receptor like-2 - mouse
ORGANISM   Mus musculus #common_name house mouse
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
          28-Feb-1997
ACCESSIONS 149341
REFERENCE   149339

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#authors   Gao, J.L.; Murphy, P.M.
#journal   J. Biol. Chem. (1995) 270:17494-17501
#title     Cloning and differential tissue-specific expression of three
           mouse beta chemokine receptor-like genes, including the
           gene for a functional macrophage inflammatory protein-1
           alpha receptor.
#cross-references MUID:95340546
#accession 149341
#status    preliminary; translated from GB/EMBL/DBJ
#molecule-type DNA
#residues  1-359 #label RES
#cross-references MUID:U28406; NID:9881551; PID:9881552
SUMMARY    #length 359 #molecular-weight 41857 #checksum 8333

Query Match      68.1%; Score 1880; DB 2; Length 359;
Best Local Similarity 68.8%; Pred. No. 1.45e-253;
Matches 240; Conservative 49; Mismatches 58; Indels 2; Gaps 2;

Db 12 VSEFTTPEYEMAP-CEKRAIKELGSMPLPPLYSLVFTIGLGNMNVVILIKRKIQ 70
    |||||
QY 8 VFTFTTST-YDDVGLCEKADTRALMAQFVPPLSLVFTVGLGNVVMILIKRRLR 66

Db 71 IMNTIYLFNLAIISDLFLFTVPFWIHVYLMNMGHGMCKMLSGFYIALYSEIFITL 130
    |||||
QY 67 IMNTIYLFNLAIISDLFLFTVPFWIHVYLMNMGHGMCKMLSGFYIALYSEIFITL 126

Db 131 LTIDRYLAIVHAFALRARTVFPATITSITWGLAGLALPEFIYEHESQDSFGFSCSPR 190
    |||||
QY 127 LTIDRYLAIVHAFALRARTVFPATITSITWGLAGLALPEFIYEHESQDSFGFSCSPR 186

Db 191 YEGSEDSMKRPHALRNMIFGALPLVMAVYCSGIIITLRCPKKKHKAIRLIFVMI 250
    |||||
QY 187 YPEDTVYSWRHFTLRMTIFCLVPLVMAICYGILIKLRPSKKKYAIRLIFVMA 246

Db 251 VFIFMTPIYVAILLSYQSILFGNDCERSKHLDRVWLVTETVAYSHCCNPVIYAFGE 310
    |||||
QY 247 VFIFMTPIYVAILLSYQSILFGNDCERSKHLDRVWLVTETVAYSHCCNPVIYAFGE 306

Db 311 RRRKHLRFHRRNVQFTWENIFQFLPGEENGRTSSVSPSTGEISVFE 359
    |||||
QY 307 RRRKHLRFHRRNLMLHGRYIPFLPSEKLERTSSVSPSTAEPLSLVF 355

RESULT      4
ENTRY      A45177      #type complete
TITLE      Chemokine (C-C) receptor 1 - human
ALTERNATE_NAMES C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
ORGANISM   Homo sapiens #common_name man
DATE       30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
          10-Sep-1997
ACCESSIONS A45177; I55671
REFERENCE   A45177
#authors   Neote, K.; Digregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
#journal   Cell (1993) 72:415-425
#title     Molecular cloning, functional expression, and signaling
           characteristics of a C-C chemokine receptor.
#cross-references MUID:93161416
#accession A45177
#status    nucleic acid sequence not shown
#molecule-type mRNA
#residues  1-355 #label NFO
#cross-references GB:U10918; NID:9292416; PID:9292417
#experimental_source HL60 cells
#note      sequence extracted from NCBI backbone (NCBIP:124876)
REFERENCE   I55671
#authors   Gao, J.
#journal   J. Exp. Med. (1993) 177:1421-1427
#title     Structure and functional expression of the human macrophage
           inflammatory 1 alpha (MIP-1alpha)/RANTES receptor.
#cross-references MUID:93240122
#accession I55671
#status    preliminary; translated from GB/EMBL/DBJ
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[illegible]

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Matches 174	Conservative	69	Mismatches 75	Indels 2
				Gaps 2
Db	56 YEESAP-CYKSDTRRLAAOVPAALYLIVLEFGLGLNLVLIIVIRYKIKNTLMNL 114			
Qy	17 YDDGLGLOEKADTRRLAAQFVPRPLSYLFTYGLGNNVVWMLIKYRRLMTNITLNT 76			
Db	115 AISDLFLFTLPFMMHITIGMTHTDTEFGISLCKLRGVCYNLSQVVCITLLIVDRILAV 174			
Qy	77 AISDLFLFTLPFMIHIV-RGHNWVFHGKMKLLSGYHGLXSEIFILLIDRLAI 135			
Db	175 VYAAVLAFFRTTGVIGVCTWFLAGLSLPEFFFGHODDNGRVCDDPYEMSTNW 234			
Qy	136 VHAFALPARKIVTGVITSIYTWGLAVLAALPEITFETELPEETLCALYEPDIYSW 195			
Db	235 RAHAAYKIMLSLIPLLINAVCYVYIIRLLRRPSKKYKAIRLIFVIMAYFVWTPY 294			
Qy	196 RHFTLRRTIECLVPLIVMAICYTGIIKTLRCPSSKKYKAIRLIFVIMAYFVWTPY 255			
Db	295 NIVLLSTFHTLNLQCALSSNIDMALITKYTAIYHCCINPIYAFVGEKRRRLHYF 354			
Qy	256 NVALISYOSILGNCDESKHLDMVLYEIVAYSHCCMPYIAVAFERFRKYLRHF 315			
Db	355 FHTYAYLYCKYIPELSDG 373			
Qy	316 FHRHLMHIGRIEPLPSE 334			
RESULT	9			
ENTRY	I49340	#type complete		
TITLE	MIP-1 alpha receptor like-1 - mouse			
ORGANISM	02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change			
DATE	28-Feb-1997			
ACCESSIONS	I49340			
REFERENCE	I49339			
#authors	Gao, J. L.; Murphy, P. M.			
#journal	J. Biol. Chem. (1995) 270:17494-17501			
#title	Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.			
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#accession	I49340			
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##molecule_type	DNA			
##residues	1-356	#label RES		
##cross-references	EMBL:028405; NID:g881549; PID:g881550			
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Best Local Similarity	52.3%	Pred. No. 2.38e-187		
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				Gaps 2
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Qy	21 GILCEKADTRRLAAQFVPRPLSYLFTYGLGNNVVWMLIKYRRLMTNITLNLAIISD 80			
Db	82 LVFLSTLPFVNDYIMKGDWIPGNACKFVSGFYLLGLYSDFITLLTIDRYLAVAVVF 141			
Qy	81 LLEFLTLPFVHWYKGNHWVGHGCKMLLSEFYHTGLYSEFILLTIDRYLAVAVVF 140			
Db	142 ALRATVTFGIISSITTVWLAALYSICLYVF-KSQMEFYHTHCRAILPKKSLIRPFRQ 200			
Qy	141 ALRATVTFGVITSIYTWGLAVLAALP-EFFETTELFEETLCALYEPDIYSWRFH 199			
Db	201 ALTNMIIILPLPLAMICITRIINVLHRRNKAKAVNRIPIYTLTFEFLAAYLYA 260			
Qy	200 TLKRTIFCVLPPLVMAICTGIITKLTRCPSKKYKAIRLIFVIMAYFVLEFMTPIYVAI 259			
Db	261 FVSAFEDVLTPTSCIRSOQVDLSMTIEALAYTHCCVNPVLYVFGRRFRKYIMQLEFRH 350			

QY 260 LSSYOSILGNDCEKSKHLDVLMVTEVIAVSHCCNMPVIAVFGERFRKYLRFHFRH 319

Db 321 TAITLPQMLPELSEDRARASARLPSEVEIETS 353

QY 320 LMLHGRYIPFLPESEKLERTSSVSPSTAEPELS 352

RESULT 10

ENTRY JC2443 #type complete

TITLE Chemokine (C-C) receptor 2, splice form B - human

ALTERNATE_NAMES C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor

ORGANISM #formal_name Homo sapiens #common_name man

DATE 21-Feb-1995 #sequence_revision 03-Apr-1995 #text_change 10-Sep-1997

ACCESSIONS JC2443 138463

REFERENCE JC2443

Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N. Biochem. Biophys. Res. Commun. (1994) 202:1156-1162

#journal Molecular cloning and functional expression of a human monocyte chemoattractant protein 1 receptor.

#accession JC2443

#molecule_type mRNA

#residues 1-360 #label YAM

REFERENCE A53477

#cross-references DBJ:029984; NID:9531246; PID:d1006817; PID:9531247

#authors Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756

#title Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

#cross-references M01D:94195821

#accession I38463

#molecule_type mRNA

#status preliminary

#residues 1-360 #label RES

GENETICS #cross-references EMBL:003905; NID:9472557; PID:9472558

#gene GDB:CMKBR2

#cross-references GDB:337364; OMIM:601267

#map_position 3p21-3p21

KEYWORDS alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

FEATURE

3-70 #domain transmembrane #status predicted #label TM1

61-100 #domain transmembrane #status predicted #label TM2

115-136 #domain transmembrane #status predicted #label TM3

154-178 #domain transmembrane #status predicted #label TM4

207-226 #domain transmembrane #status predicted #label TM5

244-268 #domain transmembrane #status predicted #label TM6

287-309 #domain transmembrane #status predicted #label TM7

14 #binding_site carbohydrate (Asn) (covalent) #status predicted

113-190 #disulfide_bonds #status predicted

SUMMARY #length 360 #molecular_weight 41063 #checksum 1732

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Best local Similarity 52.8%; Pred. No. 1,176-184;

Matches 181; Conservative 88; Mismatches 64; Indels 10; Gaps 8;

Db 21 TTFEDYDYGAPCKRPDYKQIGAOQLPPLYSLVIFEGVGNMLVVLILINCKKLKCLTDIY 80

QY 14 TSYD-DVGLCEKADTRALMAQFVPLYSVFTVGLGNVVVMILIKRRLIMINTY 72

Db 81 LNLNLAISDLFLTLPLMAHSA-ANENVFGNACKLFTGLYHGYEGGIFITLLITDRY 139

QY 73 LNLNLAISDLFLTLPLMAHSA-ANENVFGNACKLFTGLYHGYEGGIFITLLITDRY 132

Db 140 LAIVHAFALKARTVTEGVTSVITMLVAFAVSPGIIFTCCKEDSVYVCGPFP--R- 196

QY 133 LAIVHAFALKARTVTEGVTSVITMLVAFAVSPGIIFTCCKEDSVYVCGPFP--R- 192

Db 197 -GNMNFHTIRNLTGLVPLILNIVICYSGLTKLLCRNEKRRARVRYITFTMIYELF 255

QY 193 YSWRHFTIRNLTGLVPLILNIVICYSGLTKLLCRNEKRRARVRYITFTMIYELF 251

Db 256 WPEYNIIVLLNTFOEP-EGLSNCESTSQLDAQOVETIGMTGCCINPIIYAFVGEKFR 314

QY 252 WTPYNAIILSSYOSILFG-NDCEKSKHLDVLMVTEVIAVSHCCNMPVIAVFGERFRK 310

Db 315 YLSVFERKHTKRCOCQPVREYDGVTSINTPSTGEOVS 357

QY 311 YLRHFFRHILMLHGRYIPFLPESEKLE-RTSSVSPSTAEPELS 352

RESULT 11

ENTRY I38450 #type complete

TITLE Chemokine (C-C) receptor 2, splice form A - human

ALTERNATE_NAMES C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chemotactin 1 receptor

ORGANISM #formal_name Homo sapiens #common_name man

DATE 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 29-Aug-1997

ACCESSIONS I38450

REFERENCE A53477

#authors Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756

#title Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

#cross-references M01D:94195821

#accession I38450

#molecule_type mRNA

#status preliminary

#residues 1-374 #label RES

GENETICS #cross-references EMBL:003882; NID:9472555; PID:9472556

#gene GDB:CMKBR2

#cross-references GDB:337364; OMIM:601267

#map_position 3p21-3p21

KEYWORDS alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

FEATURE

44-68 #domain transmembrane #status predicted #label TM1

79-99 #domain transmembrane #status predicted #label TM2

115-136 #domain transmembrane #status predicted #label TM3

154-178 #domain transmembrane #status predicted #label TM4

208-226 #domain transmembrane #status predicted #label TM5

244-265 #domain transmembrane #status predicted #label TM6

292-309 #domain transmembrane #status predicted #label TM7

14 #binding_site carbohydrate (Asn) (covalent) #status predicted

32-277,113-190 #disulfide_bonds #status predicted

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QY 14 TSYD-DVGLCEKADTRALMAQFVPLYSVFTVGLGNVVVMILIKRRLIMINTY 72

Db 81 LNLNLAISDLFLTLPLMAHSA-ANENVFGNACKLFTGLYHGYEGGIFITLLITDRY 139

QY 73 LNLNLAISDLFLTLPLMAHSA-ANENVFGNACKLFTGLYHGYEGGIFITLLITDRY 132

Db 140 LAIVHAFALKARTVTEGVTSVITMLVAFAVSPGIIFTCCKEDSVYVCGPFP--R- 196

QY 133 LAIVHAFALKARTVTEGVTSVITMLVAFAVSPGIIFTCCKEDSVYVCGPFP--R- 192

Db 197 -GNMNFHTIRNLTGLVPLILNIVICYSGLTKLLCRNEKRRARVRYITFTMIYELF 255

QY 193 YSWRHFTIRNLTGLVPLILNIVICYSGLTKLLCRNEKRRARVRYITFTMIYELF 251

	Dd	266	MTPYIVLVITVDFEFG-GLGNSCESTQSLODAOTVEETLGTGHCCINPIIYAFAEGKRR	313
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	TITLE		C-C CKR-4	
	ALTERNATE_NAMES		#formal_name Homo sapiens #common_name man	
	ORGANISM		10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change	
	DATE		15-Aug-1997	
	ACCESSIONS		A57160	
	REFERENCE		A57160	
	#authors		Power, C.A.; Meyer, A.; Nemeth, K.J.; Bacon, K.B.; Hoogewerf,	
			A.J.; Proudfoot, A.E.L.; Wells, T.N.C.	
	#journal		J. Biol. Chem. (1995) 270:19495-19500	
	#title		Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line	
	#accession		A57160	
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	GENETICS	GDB:CMKR4		
	#gene	##cross-references GDB:677463		
	##map_position	3p21-3p21		
	KEYWORDS	G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein		
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	FEATURE			
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	76-97	#domain transmembrane #status predicted #label TM2\		
	112-133	#domain transmembrane #status predicted #label TM3\		
	151-175	#domain transmembrane #status predicted #label TM4\		
	208-226	#domain transmembrane #status predicted #label TM5\		
	243-264	#domain transmembrane #status predicted #label TM6\		
	291-308	#domain transmembrane #status predicted #label TM7\		
	29-276,110-187	#disulfide bonds #status predicted\		
	72,350	#binding_site phosphate (Ser) (covalent) (by casein kinase II) #status predicted\		
	145	#binding_site phosphate (Ser) (covalent) (by protein kinase C) #status predicted\		
	183,194	#binding_site carbohydrate (Asn) (covalent) #status predicted\		
	321	#binding_site phosphate (Thr) (covalent) (by protein kinase C) #status predicted		
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	Matches 160; Conservative 83; Mismatches 103; Indels 5; Gaps 5			
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	Oy	3	TSLDPEVFGETTSYYDDVGLCERADPRMALMAOEPFLSYLTFTGGIGNVVMIIKIY	62
	Dd	68	KRLREMTDVYLNLTAISDLLEFPVSIFPGGYAAAO-WREGIGLKMSMXYLVFYSGIF	126
	Oy	63	RRLRMNTVILLNLTAISDLLLVLPFWIHVRGNMWVFGHGCKKLGSFHTLSYEIRF	122
	Dd	127	FVMLMSIDRYLAIAHVAWSLRARLLTYVINSLATSWAASVASIPGFSEFCYERRHYT	186
	Oy	123	FIILTTRDYLAIAHVAWRARTREVITSITYTWGAIVAAALAPFRIFTTELFEETL	182
	Dd	187	CTKTYSLNST-TWKVASSLEINIQLGVIPDGIMFCYSMIIRTLOCHKNEKNRAVKMIF	245
	Oy	183	CSALTPEPTTVSSWMRFHLRTICFLVPPLVMAICYGITIKTLRPCSKKKYAKRIIE	242
	Dd	246	AVVVVLGFQMPPYNIVLFLLEVLEVDIOCTFERFYEDYALOAFETLAFVHCCLNPITIF	305
	Oy	:	: : : : : : : : :	:

OY	243	VIMAVFEFMPVVAVALISSYOSILFGNDCKERSKHLDMVLTEVIAYASHCCMNPVITA	302
Db	306	FLGEFKRYIIQLQETCRGLFVLCQYCGLLQIYSADTPSSSYOSTMDHDL	356
OY	303	FVGGRFRKYRLNHFPHR-HLMLHGORYIPFLPSKLE-RITSVSPTAEPEL	351
RESULT	13		
ENTRY	JC4587	#type complete	
TITLE	Chemokine (C-C) receptor 4 - mouse		
ORGANISM	#formal_name Mus musculus #common_name house mouse		
DATE	08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 12-Dec-1997		
ACCESSIONS	JC4587		
REFERENCE	JC4587		
authors	Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C. Power, C.A.		
#journal	Molecem. Biophys. Res. Commun. (1996) 218:337-343		
#title	Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to murine and human CC CKR-4.		
#accession	JC4587		
##molecule_type mRNA			
##residues	1-360 #label HOO		
##cross-references EMBL:X80862; NID:g167851; PID:e195632; PID:g167852			
##experimental_source thymus			
GENETICS			
#gene	cc ckr-4		
KEYWORDS	glycoprotein; phosphoprotein; receptor; thymus		
FEATURE			
2,183,194	#binding_site carbohydrate (Asn) (covalent) #status predicted\		
72,202,350	#binding_site phosphate (Ser) (covalent) (by casein kinase II) #status predicted\		
145	#binding_site phosphate (Ser) (covalent) (by protein kinase C) #status predicted\		
321	#binding_site phosphate (Thr) (covalent) (by protein kinase C) #status predicted		
SUMMARY	#length 360 #molecular_weight 41462 #checksum 7852		
Query Match	43.4%; Score 1199; DB 2; Length 360;		
Best Local Similarity	43.7%; Pred. No. 1,41e-151;		
Matches 150; Conservative 92; Mismatches 97; Indels 4; Gaps 4;			
Db	16 YNSTYFFESMPKPKCTKGKIKAFGEVLPPLSLVFLLGFGNSVVVLFKKYRLKMSMTD	75	
OY	11 FGTSTYDDVGLCEKADTRALMAQEFPPPLYSLVFETGLGNVVVMILTKYRLRIRMTN	70	
Db	76 VYLNLAIISDLIFVLSLFPWGYAAAD-QWEFGLGCKIVGMMVLGVGFSGIFPMASID	134	
OY	71 IYLNLAISDLIFVLTLPFWIHVRGHNVFGHMCLSLGFYHTGISIFPITILLTD	130	
Db	135 RYLAIVHAVESLKARTLYGVTSILTWSVAVPASLPGILFTSTCYTEHNHTYCKTOYSVN	194	
OY	131 RYLAIVHAVFALARVTGFGVITSYTWGLAVLAALPELFFEYTEDELFEETLCSALYPED	190	
Db	195 ST-TWKVLSSEINVLCLLPGLIMLFWMISMITRILOHCNEKNKNAVRMGSVVVLFIG	253	
OY	191 TVYSWRHRTLRMTIFCLVPLPYMAAICYGIIITKLRCPSKKRYKAIRLIFFVIMAVFEI	250	
Db	254 FWEPYNVVLFEETVELVEVDQCTLBKXYLXAQARETIGFINHCNPNPVYFFLGKPKR	313	
OY	251 FWTPYNAVAILLSYQSILFGNDESRSHLDLMVLVEVLAISHCCMNPIYAVGGERPK	310	
Db	314 YITOLFRCRPVLCLKHCDPLQVYASADMSSSYSTVDHDF	356	
OY	311 YLRHFFHR-HLMLHGLRYIPFLPSKEKRISV-SPTAEPEL	351	
RESULT	14		
ENTRY	JC5067	#type complete	
TITLE	G protein-coupled receptor CKR-11 - human		
ALTERNATE_NAMES	Chemokine receptor-like protein TER1; GPR-Cy6		
ORGANISM	#formal_name Homo sapiens #common_name man		

DATE 31-Jan-1997 #sequence-revision 31-Jan-1997 #text_change
10-Sep-1997
ACCESSIONS J05067; G02776; G02387
REFERENCE J05067
#authors Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
#journal Biochem. Biophys. Res. Commun. (1996) 227:846-853
#title Molecular cloning and RNA expression of two new human chemokine receptor-like genes.
#accession J05067
#molecule_type DNA
#residues 1-355 #label ZAB
#cross-references EMBL:279782; NID:g1668735; PID:e264772; PID:g1668736
REFERENCE H01714
#authors Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
#journal Submitted to the EMBL Data Library, June 1996
#accession G02776
#molecule_type DNA
#residues 1-355 #label NAP
#cross-references EMBL:062556; NID:g1468978; PID:g1468979
REFERENCE H01154
#authors Bonner, T.I.
#submitted to the EMBL Data Library, January 1996
#accession G02387
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-355 #label BON
#cross-references EMBL:045983; NID:g1245057; PID:g1245057
COMMENT This protein belongs to the family of beta chemokine receptors.
GENETICS
#gene TER1
KEYWORDS G protein-coupled receptor; transmembrane protein
FEATURES
36-63 #domain transmembrane #status predicted #label TM1
73-94 #domain transmembrane #status predicted #label TM2
108-129 #domain transmembrane #status predicted #label TM3
147-171 #domain transmembrane #status predicted #label TM4
200-222 #domain transmembrane #status predicted #label TM5
239-260 #domain transmembrane #status predicted #label TM6
281-304 #domain transmembrane #status predicted #label TM7
SUMMARY #length 355 #molecular-weight 40844 #checksum 2562
Query Match 38.7%; Score 1067; DB 2; Length 355;
Best Local Similarity 39.1%; Pred. No. 5,11e-132;
Matches 133; Conservative 96; Mismatches 103; Indels 8; Gaps 6;
Db 1 MDYTLDSVTYTDVYYPDFSSPCDAELIQNGKLLAVFCLFVBSLNSLYIVL 60
QY 1 MTSIDTVEFTCTSYDDV-GULCEKADTRALMAQFVPLSLVFTVGLGNVVMIL 59
Db 61 VVCKRLRSITDVYLLNLALSDLLFVSPFQTYLLDQ-WVFGTVACKVVGFEYIGFYS 119
QY 60 IYRRRLRITNTIYLLNLALSDLLFVTLFPWIIHYVGNHNVFGHGCKRLISGFYHGLIS 119
Db 120 SNEFTLMSVDRLAVNAVAVALKVFTRMGTTLCIAVNLTAIMATIPLLVEYQVASE-D 178
QY 120 EIFFIILLIDRYLAIVHAFVAFALRAFTVFGVITSIVTWGLAVLALPEFIYEELFE 179
Db 179 GVLQCYSEFNQOGL-KWKFTNFKNIIGLLIPFTIFMFCYIKILHQLKRCQNHKTKAI 237
QY 180 ETL-CSALPDPEDIVSWRFHFLRMITFCLVPLLVMAICYTGIIKTLRCPSKRRYKAI 238
Db 238 RLVLIVINSLFWPFPNVFLTSLSHMILDGCSISQQLFYATFHEIISFTGCCVNP 297
QY 239 RLIFVIMAVFIFFWPYNAIILSSVQSLIFGNDCCRSKHLDMYLVTVIAYSHCCAMP 298
Db 298 VYFAVGEKFKKHLSEIFOKSCQIFNYLGRQMPRESCEK 337
QY 299 VYFAVGERFRKRYLRHFHR--HLMLHGRYIPLPSEK 335

RESULT 15
ENTRY I58186 #type complete
TITLE hypothetical G-protein coupled receptor - rat
ORGANISM Rattus norvegicus #common_name Norway rat
DATE 26-Jul-1996 #sequence-revision 26-Jul-1996 #text_change 30-May-1997
ACCESSIONS I58186
REFERENCE I58186
#authors Harrison, J.K.; Barber, C.M.; Lynch, K.R.
#journal Neurosci. Lett. (1994) 169:85-89
#title cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and brain related to chemokine receptors.
#cross-references MUID:94323113
#accession I58186
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-354 #label RES
#cross-references EMBL:044808; NID:g439860; PID:g439861
KEYWORDS G protein-coupled receptor
SUMMARY #length 354 #molecular-weight 40327 #checksum 4478
Query Match 38.4%; Score 1059; DB 2; Length 354;
Best Local Similarity 44.8%; Pred. No. 7.78e-131;
Matches 139; Conservative 77; Mismatches 89; Indels 5; Gaps 4;
Db 15 YDSSAEACYLGDYVAGTIFLFSYSLVFTGLVGNLLVLAINSRKSITDIYLLNL 74
QY 17 YDDVGLCEKADTRALMAQFVPLSLVFTVGLGNVVMILIKYRRLRITNTIYLLNL 76
Db 75 ALSDLLFVATLPFWTHYLSHE-GLHNMCKLTNAFFIGFGGFFFTVISIDRYLAI 133
QY 77 ALSDLLFVATLPFWTHYLSHE-GLHNMCKLTNAFFIGFGGFFFTVISIDRYLAI 136
Db 134 LAANSNNRRTVOHGVTISLGVAAAILVASPOFMETKRD--NECL-GD-YPEVLQETIP 189
QY 137 HAVFLRARTVFGVITSIVTWGLAVLALPEFIYEELFEELCSALPDPEDIVSWR 196
Db 190 VLRSEVNIIGVPLPLMSFCYFRIVTFLSCNKKRAIRLLVAVVFFLEWTPYN 249
QY 197 HHFTLRMTIFCIVLPLVMAICYTGIIKTLRCPSKRRYKAIRLFVIMAVFIFWTPYN 256
Db 250 IYIPELTLEFNFSPGCMKRDRLVALSVTEFVAFSHCCLPFTIYAFGEKFRRLRLX 309
QY 257 VALLSYQSILFGNDCRSKHLDMLVTEVIAVSHCCAMPVYAFVGERFRKRYLRHF 316
Db 310 NKCLAVLCGR 319
QY 317 HRHLLMHGR 326
Search completed: Tue Dec 8 13:19:14 1998
Job time : 63 secs.

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